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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

on: Tue Apr 20 13:57:56 1999; MasPar time 4.85 seconds
                                       174.525 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-836-455-2
Perfect Score: (50-66) from US08836455.pep (2 of 3)
Sequence: 131
                   1 GINLHWLQQEPDGTIKR 17

Scoring table: PAM 150
                   Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%
                   Listing first 45 summaries

Database: sptremb16
                   1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
                   5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
                   9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
                   13:sp_vertebrate 14:sp_virus

Statistics: Mean 27.617; Variance 43.342; scale 0.637

                   Pred. No. is the number of results predicted by chance to have a
                   score greater than or equal to the score of the result being printed,
                   and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	73	55.7	426	2	Q47315	TRANSPOSASE IS91.	6.71e-02
2	69	52.7	365	14	O86302	SIGMA 3.	3.47e-01
3	69	52.7	365	14	O86293	SIGMA 3.	3.47e-01
4	69	52.7	365	14	O86301	SIGMA 3.	3.47e-01
5	69	52.7	365	14	O86297	SIGMA 3.	3.47e-01
6	69	52.7	365	14	O86294	SIGMA 3.	3.47e-01
7	69	52.7	365	14	O86299	SIGMA 3.	3.47e-01
8	69	52.7	365	14	O86296	SIGMA 3.	3.47e-01
9	69	51.9	455	10	O64733	PUTATIVE INDOLE-3-ACET	5.19e-01
10	68	50.4	238	10	O23300	CARNITINE RACEMASE HOM	1.15e+00
11	66	50.4	356	14	O82515	HEMAGGLUTININ PRECURSO	1.15e+00
12	66	50.4	365	14	O98642	OUTER-CAPSID PROTEIN S	1.15e+00
13	66	50.4	365	14	O98640	OUTER-CAPSID PROTEIN S	1.15e+00
14	66	50.4	365	14	O98639	OUTER-CAPSID PROTEIN S	1.15e+00
15	66	50.4	365	14	O98641	OUTER-CAPSID PROTEIN S	1.15e+00
16	66	50.4	365	14	O86300	SIGMA 3.	1.15e+00
17	66	50.4	365	14	O86295	SIGMA 3.	1.15e+00
18	66	50.4	365	14	O98638	OUTER-CAPSID PROTEIN S	1.15e+00
19	66	50.4	365	14	O86303	SIGMA 3.	1.15e+00
20	66	50.4	365	14	O98827	OUTER-CAPSID PROTEIN S	1.15e+00
21	66	50.4	365	14	O86292	SIGMA 3.	1.15e+00
22	66	50.4	365	14	O86291	SIGMA 3.	1.15e+00
23	65	49.6	136	4	O43725	DJ29K1.1.	1.70e+00
24	65	49.6	563	14	O84027	INFLUENZA A/FPV/ROSTOC	1.70e+00
25	65	48.1	563	14	O67087	INFLUENZA A/FPV/	1.70e+00
26	63	48.1	361	14	O82507	HEMAGGLUTININ PRECURSO	3.70e+00
27	63	48.1	362	14	O82513	HEMAGGLUTININ PRECURSO	3.70e+00
28	63	48.1	362	14	O82516	HEMAGGLUTININ PRECURSO	3.70e+00
29	63	48.1	365	14	O86298	SIGMA 3.	3.70e+00
30	63	48.1	373	14	O82519	SIGMA 3.	3.70e+00
31	63	48.1	560	14	O82518	HEMAGGLUTININ PRECURSO	3.70e+00
32	63	48.1	562	14	O82514	HEMAGGLUTININ PRECURSO	3.70e+00
33	63	48.1	562	14	O82562	HEMAGGLUTININ PRECURSO	3.70e+00
34	63	48.1	562	14	O82511	HEMAGGLUTININ PRECURSO	3.70e+00
35	63	48.1	562	14	O82508	HEMAGGLUTININ PRECURSO	3.70e+00
36	63	48.1	563	14	O82564	HEMAGGLUTININ PRECURSO	3.70e+00
37	63	48.1	564	14	O82563	HEMAGGLUTININ PRECURSO	3.70e+00
38	63	48.1	697	5	O61121	RNA GUANYLYLTRANSFERAS	3.70e+00
39	63	47.3	322	2	O62266	REGION B OF COSMID SCY	5.42e+00
40	62	47.3	362	14	O82517	HEMAGGLUTININ PRECURSO	5.42e+00
41	62	47.3	543	14	O55114	MULTIGENE FAMILY 530 P	5.42e+00
42	62	47.3	763	2	O60013	DNA TOPOISOMERASE I.	5.42e+00
43	62	47.3	985	13	O91571	RECEPTOR TYROSINE KINA	5.42e+00
44	61	46.6	370	14	O82512	HEMAGGLUTININ PRECURSO	7.91e+00
45	61	46.6	545	14	Q64967	VIRAL FUSION PROTEIN (	7.91e+00

ALIGNMENTS

```
RESULT   1
ID   Q47315            PRELIMINARY;      PRT;     426 AA.
AC   Q47315;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   TRANSPOSASE IS91.
GN   TNPA.
OS   ESCHERICHIA COLI.
OG   PLASMID PSU2911.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   ENTEROBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92138630.
RA   MENDIOLA M.V., JUBETE Y., LA CRUZ F.;
RL   J. BACTERIOL. 174:1345-1351(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92335017.
RA   MENDIOLA M.V., DE LA CRUZ F.;
RL   NUCLEIC ACIDS RES. 20:3521-3521(1992).
DR   EMBL; X17114; G41842; -.
KW   PLASMID.
SQ   SEQUENCE    426 AA;    49982 MW;    226BE3E5 CRC32;

Query Match    55.7%;  Score 73;  DB 2;  Length 426;
Best Local Similarity  38.5%;  Pred. No. 6.71e-02;
Matches    5;  Conservative   7;  Mismatches   1;  Indels   0;  Gaps   0;

Db        16 LNWLEKQPEGSSVR 28
             |:||:|:||:|:||:
Qy        53 LHWLQQEPDGTIK 65


RESULT   2
ID   O86302            PRELIMINARY;      PRT;     365 AA.
AC   O86302;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   SIGMA 3.
GN   S4.
OS   REOVIRUS.
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OC   VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95074914.
RC   STRAIN=SEROTYPE 3;
RA   KEDL R., SCHMECHEL S.C., SCHIFF L.A.;
RL   J. VIROL. 69:552-559(1995).
DR   EMBL; U15083; G706880; -.
SQ   SEQUENCE 365 AA; 594C3CEF CRC32;

Query Match          52.7%;  Score 69;  DB 14;  Length 365;
Best Local Similarity 40.0%;  Pred. No. 3.47e-01;
Matches    6;  Conservative   7;  Mismatches   2;  Indels   0;  Gaps   0;

Qy    51 INLHWLQQEPDGTIK 65
         ::|:|||:||::::
Db   129 VELNWLQVPDSMFR 143


RESULT 3
ID   Q86293      PRELIMINARY;      PRT;   365 AA.
AC   Q86293;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   SIGMA 3.
GN   S4.
OS   REOVIRUS.
OC   VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SEROTYPE 3;
RX   MEDLINE; 95074914.
RA   KEDL R., SCHMECHEL S.C., SCHIFF L.A.;
RL   J. VIROL. 69:552-559(1995).
DR   EMBL; U15074; G706862; -.
SQ   SEQUENCE 365 AA; 41032 MW; D074A4E4 CRC32;

Qy    51 INLHWLQQEPDGTIK 65
         :||:||| :||: ::
Db   129 VELNWLQVPDSMFR 143

Query Match          52.7%;  Score 69;  DB 14;  Length 365;
Best Local Similarity 40.0%;  Pred. No. 3.47e-01;
Matches    6;  Conservative   7;  Mismatches   2;  Indels   0;  Gaps   0;


RESULT 4
ID   Q86301      PRELIMINARY;      PRT;   365 AA.
AC   Q86301;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   SIGMA 3.
GN   S4.
OS   REOVIRUS.
OC   VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SEROTYPE 3;
RX   MEDLINE; 95074914.
RA   KEDL R., SCHMECHEL S.C., SCHIFF L.A.;
RL   J. VIROL. 69:552-559(1995).
DR   EMBL; U15082; G706878; -.
SQ   SEQUENCE 365 AA; 41123 MW; 1A54DC7D CRC32;

Query Match          52.7%;  Score 69;  DB 14;  Length 365;
Best Local Similarity 40.0%;  Pred. No. 3.47e-01;
Matches    6;  Conservative   7;  Mismatches   2;  Indels   0;  Gaps   0;

Db   129 VELNWLQVPDSMFR 143
         ::|:||| :||: ::
Qy    51 INLHWLQQEPDGTIK 65


RESULT 5
ID   Q86297      PRELIMINARY;      PRT;   365 AA.
AC   Q86297;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   SIGMA 3.
GN   S4.
OS   REOVIRUS.
OC   VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SEROTYPE 3;
RX   MEDLINE; 95074914.
RA   KEDL R., SCHMECHEL S.C., SCHIFF L.A.;
RL   J. VIROL. 69:552-559(1995).
DR   EMBL; U15078; G706870; -.
SQ   SEQUENCE 365 AA; 41018 MW; 139ED362 CRC32;

Query Match          52.7%;  Score 69;  DB 14;  Length 365;
Best Local Similarity 40.0%;  Pred. No. 3.47e-01;
Matches    6;  Conservative   7;  Mismatches   2;  Indels   0;  Gaps   0;

Qy    51 INLHWLQQEPDGTIK 65
         ::|:||| :||: ::
Db   129 VELNWLQVPDSMFR 143


RESULT 6
ID   Q86294      PRELIMINARY;      PRT;   365 AA.
AC   Q86294;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   SIGMA 3.
GN   S4.
OS   REOVIRUS.
OC   VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SEROTYPE 1;
RX   MEDLINE; 95074914.
RA   KEDL R., SCHMECHEL S.C., SCHIFF L.A.;
RL   J. VIROL. 69:552-559(1995).
DR   EMBL; U15075; G706864; -.
SQ   SEQUENCE 365 AA; 40993 MW; 251F3243 CRC32;

Qy    51 INLHWLQQEPDGTIK 65
         ::|:||| :||: ::
Db   129 VELNWLQVPDSMFR 143

Query Match          52.7%;  Score 69;  DB 14;  Length 365;
Best Local Similarity 40.0%;  Pred. No. 3.47e-01;
Matches    6;  Conservative   7;  Mismatches   2;  Indels   0;  Gaps   0;


RESULT 7
ID   Q86299      PRELIMINARY;      PRT;   365 AA.
AC   Q86299;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   SIGMA 3.
GN   S4.
OS   REOVIRUS.
OC   VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SEROTYPE 3;
RX   MEDLINE; 95074914.
RA   KEDL R., SCHMECHEL S.C., SCHIFF L.A.;
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RL   J. VIROL. 69:552-559(1995).
DR   EMBL; U15080; G706874; -.
SQ   SEQUENCE   365 AA;   41074 MW;  0B2EE93D CRC32;

Query Match             52.7%;  Score 69;  DB 14;  Length 365;
Best Local Similarity   40.0%;  Pred. No. 3.47e-01;
Matches    6;  Conservative   7;  Mismatches   2;  Indels   0;  Gaps   0;

Qy   51 INLHWLQQEPDGTIK 65
        :::|::|||:|||: ::
Db  129 VELNWLQVDDSMFR 143


RESULT 8
ID   Q86296              PRELIMINARY;   PRT;   365 AA.
AC   Q86296;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   SIGMA 3.
OS   S4.
OS   REOVIRUS.
OC   VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN-SEROTYPE 3;
RX   MEDLINE; 95074914.
RA   KEDL R., SCHMECHEL S.C., SCHIFF L.A.;
RL   J. VIROL. 69:552-559(1995).
DR   EMBL; U15077; G706868; -.
SQ   SEQUENCE   365 AA;   41090 MW;  58C38B31 CRC32;

Query Match             52.7%;  Score 69;  DB 14;  Length 365;
Best Local Similarity   40.0%;  Pred. No. 3.47e-01;
Matches    6;  Conservative   7;  Mismatches   2;  Indels   0;  Gaps   0;

Qy   51 INLHWLQQEPDGTIK 65
        :::|::|||:|||: ::
Db  129 VELNWLQVDDSMFR 143


RESULT 9
ID   Q64733              PRELIMINARY;   PRT;   455 AA.
AC   Q64733;
DT   01-AUG-1998 (TREMBLREL. 07, CREATED)
DT   01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   PUTATIVE INDOLE-3-ACETATE BETA-GLUCOSYLTRANSFERASE.
GN   T27E13.12.
OS   ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC   EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC   CAPPARALES; CRUCIFERAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN-CV. COLUMBIA;
RA   ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
RA   SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
RA   SOMERVILLE C.R., VENTER J.C.;
RL   SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AC004165; G3150406; -.
KW   TRANSFERASE.
SQ   SEQUENCE   455 AA;   51728 MW;  7C1FB50D CRC32;

Query Match             51.9%;  Score 68;  DB 10;  Length 455;
Best Local Similarity   33.3%;  Pred. No. 5.19e-01;
Matches    4;  Conservative   8;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   53 LHWLQQEPDGTI 64
        :|:|||:|:|: :
Db  260 IQWLEEQPEGSSV 271


RESULT 10
ID   Q23300              PRELIMINARY;   PRT;   238 AA.
AC   Q23300;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   CARNITINE RACEMASE HOMOLOG.
OS   ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC   EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC   CAPPARALES; CRUCIFERAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   BEVAN M., STIEKEMA W., MURPHY G., WAMBUTT R., POHL T., TERRYN N.,
RA   KREIS M., KAVANAGH T., ENTIAN K.D., RIEGER M., JAMES R.,
RA   PUIGDOMENECH P., HATZOPOULOS P., OBERMAIER B., DUESTERHOFT A.,
RA   JONES J., PALME K., ANSORGE W., DELSENY M., BANCROFT I., MEWES H.W.,
RA   SCHUELLER C., CHALWATZIS N.;
RL   SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE FROM N.A.
RP   EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
RL   SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; Z97335; E327452; -.
DR   PFAM; PF00378; ECH.
SQ   SEQUENCE   238 AA;   25595 MW;  AF74F9CD CRC32;

Query Match             50.4%;  Score 66;  DB 10;  Length 238;
Best Local Similarity   47.1%;  Pred. No. 1.15e+00;
Matches    8;  Conservative   3;  Mismatches   6;  Indels   0;  Gaps   0;

Qy   60 GFDLAWAQSAGHGAIKR 76
        :|:| :  |:|:|| |||
Db   50 GINLHWLQQEPDGTIKR 66


RESULT 11
ID   Q82515              PRELIMINARY;   PRT;   356 AA.
AC   Q82515;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   HEMAGGLUTININ PRECURSOR (FRAGMENTS).
OS   INFLUENZA A VIRUS.
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN-A/TURKEY/MINNESOTA/1237/80 (H7N3);
RX   MEDLINE; 95297170.
RA   ROHM C., HORIMOTO T., KAWAOKA Y., SUSS J., WEBSTER R.G.;
RL   VIROLOGY 209:664-670(1995).
DR   EMBL; U20466; G902767; -.
DR   PFAM; PF00509; Hemagglutinin.
KW   SIGNAL.
FT   SIGNAL         1      18
FT   CHAIN         19    >339       POTENTIAL.
FT   NON_CONS     339     340       HEMAGGLUTININ 1 CHAIN.
FT   CHAIN        340    >356
FT   NON_TER      356     356       HEMAGGLUTININ 2 CHAIN.
SQ   SEQUENCE   356 AA;   38596 MW;  4C593717 CRC32;

Query Match             50.4%;  Score 66;  DB 14;  Length 356;
Best Local Similarity   42.9%;  Pred. No. 1.15e+00;
Matches    6;  Conservative   5;  Mismatches   3;  Indels   0;  Gaps   0;

Qy   51 INLHWLQQEPDGTI 64
        |:|:|||::|:: :
Db  239 IDFHWLLLDPNDTV 252


RESULT 12
ID   Q98642              PRELIMINARY;   PRT;   365 AA.
AC   Q98642;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
```

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DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   OUTER-CAPSID PROTEIN SIGMA 3.
GN   S4.
OS   REOVIRUS.
OC   VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=L/T2+C;
RA   WETZEL J.D., WILSON G.J., BAER G.S., DUNNIGAN L.R., WRIGHT J.P.,
RA   TANG D.S., DERMODY T.S.;
RL   SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U63309; G1518832; -.
SQ   SEQUENCE   365 AA;  40989 MW;  5B158A9C CRC32;
Qy

Query Match          50.4%;  Score  66;  DB  14;  Length 365;
Best Local Similarity  33.3%;  Pred. No. 1.15e+00;
Matches    5;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

   129  VELNWLQVDPNSMFR  143
        ::|:||| :|::: ::
    51  INLHWLQOEPDGTIK  65
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RESULT  13
ID   Q98640      PRELIMINARY;      PRT;   365 AA.
AC   Q98640;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   OUTER-CAPSID PROTEIN SIGMA 3.
GN   S4.
OS   REOVIRUS.
OC   VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=L/C;
RA   WETZEL J.D., WILSON G.J., BAER G.S., DUNNIGAN L.R., WRIGHT J.P.,
RA   TANG D.S., DERMODY T.S.;
RL   SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U63307; G1518828; -.
SQ   SEQUENCE   365 AA;  41032 MW;  3F472E32 CRC32;
Qy    51  INLHWLQOEPDGTIK  65

Query Match          50.4%;  Score  66;  DB  14;  Length 365;
Best Local Similarity  33.3%;  Pred. No. 1.15e+00;
Matches    5;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

Db  129  VELNWLQVDPNSMFR  143
         ::|:||| :|::: ::
Qy   51  INLHWLQOEPDGTIK  65
```

```
RESULT  14
ID   Q98639      PRELIMINARY;      PRT;   365 AA.
AC   Q98639;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   OUTER-CAPSID PROTEIN SIGMA 3.
GN   S4.
OS   REOVIRUS.
OC   VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PI1A1;
RA   WETZEL J.D., WILSON G.J., BAER G.S., DUNNIGAN L.R., WRIGHT J.P.,
RA   TANG D.S., DERMODY T.S.;
RL   SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U63306; G1518826; -.
SQ   SEQUENCE   365 AA;  41061 MW;  1AE1ACD8 CRC32;

Query Match          50.4%;  Score  66;  DB  14;  Length 365;
Best Local Similarity  33.3%;  Pred. No. 1.15e+00;
Matches    5;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   51  INLHWLQOEPDGTIK  65
```

```
RESULT  15
ID   Q98641      PRELIMINARY;      PRT;   365 AA.
AC   Q98641;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   OUTER-CAPSID PROTEIN SIGMA 3.
GN   S4.
OS   REOVIRUS.
OC   VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=L/T2+T3;
RA   WETZEL J.D., WILSON G.J., BAER G.S., DUNNIGAN L.R., WRIGHT J.P.,
RA   TANG D.S., DERMODY T.S.;
RL   SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U63308; G1518830; -.
SQ   SEQUENCE   365 AA;  41080 MW;  D4C19A6F CRC32;

Query Match          50.4%;  Score  66;  DB  14;  Length 365;
Best Local Similarity  33.3%;  Pred. No. 1.15e+00;
Matches    5;  Conservative    8;  Mismatches    2;  Indels    0;  Gaps    0;

Db  129  VELNWLQVDPNSMFR  143
         ::|:||| :|::: ::
Qy   51  INLHWLQOEPDGTIK  65
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Search completed: Tue Apr 20 13:58:25 1999
Job time : 29 secs.
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(TM)

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 20 14:01:43 1999; MasPar time 2.77 Seconds
              52.574 Million cell updates/sec

Tabular output not generated.

Title: >US-08-836-455-2
Description: (99-107) from US08836455.pep (3 of 3)
Sequence: 1 ESEDVFAY 9
Perfect Score: 68
Sequence: 1 ESEDVFAY 9

Scoring table: PAM 150
               Gap 11

Searched: 13922 seqs, 16180660 residues
Post-processing: Minimum Match 0%
               Listing first 45 summaries

Database: a-geneseq32
  1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
  8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29

Statistics: Mean 17.346; Variance 70.819; scale 0.245

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

## SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 68 | 100.0 | 145 | 25 | W27119 | Murine monoclonal ant | 1.06e+01 |
| 2 | 64 | 94.1 | 90 | 16 | W80078 | Mouse derived light c | 2.34e+01 |
| 3 | 64 | 94.1 | 107 | 14 | R78972 | Light chain variable | 2.34e+01 |
| 4 | 64 | 94.1 | 107 | 14 | R79247 | Light chain variable | 2.34e+01 |
| 5 | 64 | 94.1 | 108 | 4 | R79250 | Light chain variable | 2.34e+01 |
| 6 | 64 | 94.1 | 108 | 4 | R21310 | Light chain of Mif cl | 2.34e+01 |
| 7 | 64 | 94.1 | 146 | 4 | P30251 | Sequence of the leade | 2.34e+01 |
| 8 | 64 | 94.1 | 243 | 18 | W00280 | 520C9 anti-c-erbb-2 t | 2.34e+01 |
| 9 | 64 | 94.1 | 246 | 8 | R39569 | Sequence of 520C9 SFV | 2.34e+01 |
| 10 | 64 | 94.1 | 534 | 8 | R39571 | Sequence of G-FIT. | 2.34e+01 |
| 11 | 61 | 89.7 | 255 | 16 | R92829 | C179FV-PP variable 11 | 4.22e+01 |
| 12 | 61 | 89.7 | 392 | 16 | R92829 | scFv-PP. | 4.22e+01 |
| 13 | 58 | 85.3 | 98 | 16 | R82826 | Variable light region | 7.56e+01 |
| 14 | 57 | 83.8 | 90 | 16 | R80079 | Mouse derived light c | 9.17e+01 |
| 15 | 57 | 83.8 | 107 | 28 | W31726 | Alpha light chain am1 | 9.17e+01 |
| 16 | 57 | 83.8 | 107 | 25 | W27121 | Murine antibody light | 9.17e+01 |
| 17 | 57 | 83.8 | 109 | 18 | R52030 | Light chain variable | 9.17e+01 |
| 18 | 57 | 83.8 | 111 | 5 | R25721 | Humanised VL region o | 9.17e+01 |
| 19 | 57 | 83.8 | 127 | 6 | R32125 | Anti-IL2R alpha antib | 9.17e+01 |
| 20 | 57 | 83.8 | 129 | 24 | W22537 | Murine anti-human cla | 9.17e+01 |
| 21 | 57 | 83.8 | 144 | 3 | R15322 | IL-2 chimeric antibod | 9.17e+01 |
| 22 | 57 | 83.8 | 144 | 3 | R15321 | IL-2 chimeric antibod | 9.17e+01 |
| 23 | 57 | 82.4 | 107 | 29 | W44122 | Light chain variable | 9.17e+01 |
| 24 | 56 | 82.4 | 246 | 8 | R40924 | Protein able to bind | 1.11e+02 |
| 25 | 56 | 82.4 | 715 | 15 | R80482 | Recombinant bovine ad | 1.11e+02 |
| 26 | 55 | 80.9 | 82 | 16 | R93006 | Homologous sequences | 1.34e+02 |
| 27 | 55 | 80.9 | 110 | 16 | R93007 | Humanised antibody IO | 1.34e+02 |
| 28 | 55 | 80.9 | 126 | 12 | R62675 | Humanised light | 1.34e+02 |
| 29 | 55 | 80.9 | 126 | 8 | R62677 | PB1.3/Humanised light | 1.34e+02 |
| 30 | 55 | 80.9 | 126 | 12 | R62674 | CY1748RLD VL region. | 1.34e+02 |
| 31 | 55 | 80.9 | 126 | 12 | R62676 | CY1748RLC VL region. | 1.34e+02 |
| 32 | 55 | 80.9 | 126 | 12 | R43692 | CY1748RLA VL region. | 1.34e+02 |
| 33 | 55 | 79.4 | 116 | 28 | R43691 | CY1748RLB VL region. | 1.34e+02 |
| 34 | 55 | 79.4 | 104 | 28 | W31723 | PB1.3/Humanised light | 1.34e+02 |
| 35 | 54 | 79.4 | 106 | 28 | W31722 | Alpha light chain am1 | 1.63e+02 |
| 36 | 54 | 79.4 | 111 | 9 | R47492 | Alpha light chain am1 | 1.63e+02 |
| 37 | 54 | 79.4 | 115 | 28 | W41144 | Human vkappa65.3 frag | 1.63e+02 |
| 38 | 54 | 79.4 | 115 | 28 | W41145 | Human vkappa65.5 frag | 1.63e+02 |
| 39 | 54 | 79.4 | 116 | 28 | W41146 | Human vkappa65.8 frag | 1.63e+02 |
| 40 | 54 | 79.4 | 117 | 29 | W47582 | Human monoclonal anti | 1.63e+02 |
| 41 | 54 | 79.4 | 150 | 29 | W40069 | Human monoclonal anti | 1.63e+02 |
| 42 | 54 | 79.4 | 214 | 29 | W45517 | NANDC-2 light chain. | 1.63e+02 |
| 43 | 54 | 79.4 | 304 | 29 | W40071 | Human Hil-scFv constr | 1.63e+02 |
| 44 | 54 | 79.4 | 304 | 29 | W40070 | Human Hil-scFv constr | 1.63e+02 |
| 45 | 54 | 79.4 | 504 | 27 | W36140 | Bovine P58 protein. | 1.63e+02 |

## ALIGNMENTS

```
RESULT 1
ID   W27119 standard; Protein; 145 AA.
AC   W27119;
DT   04-JAN-1998 (first entry)
DE   Murine monoclonal anti-idiotype antibody 11D10 VL region.
KW   human monoclonal anti-idiotype antibody; anti-idiotype antibody; mucin;
KW   Monoclonal antibody 11D10; anti-idiotype antibody; tumour; breast cancer; vaccine.
OS   Mus musculus.
OS   human milk fat globule; HMFG; tumour; breast cancer; vaccine.
FH   Key            Location/Qualifiers
FT   Peptide        1..20
FT                  /label= Sig_peptide
FT   Protein        21..145
FT                  /label= Mat_protein
FT   Region         21..43
FT                  /label= FR1
FT                  /note= "framework region 1"
FT   Region         44..54
FT                  /label= CDR1
FT                  /note= "complementarity determining region 1"
FT   Region         55..69
FT                  /label= FR2
FT                  /note= "framework region 2"
FT   Region         70..76
FT                  /label= CDR2
FT                  /note= "complementarity determining region 2"
FT   Region         77..108
FT                  /label= FR3
FT                  /note= "framework region 3"
FT   Region         109..117
FT                  /label= CDR3
FT                  /note= "complementarity determining region 3"
FT   Region         118..127
FT                  /label= FR4
FT                  /note= "framework region 4"
PN   WO9722699-A2.
PD   26-JUN-1997.
PF   26-JUN-1996; US-575762.
PR   19-DEC-1996; U20757.
PR   13-DEC-1996; US-575762.
PR   20-DEC-1995; US-575762.
PR   20-DEC-1995; US-591965.
PR   26-JAN-1996; US-591965.
PA   (KENT ) UNIV KENTUCKY.
PA   Chatterjee M, Chatterjee SK, Foon KA;
```

DR WPI; 97-341690/31.
DR N-PSDB; T85149.
PT Monoclonal anti-idiotype antibody 11D10 - elicits immune response
PT against human milk fat globule disease associated tumours,
PT especially breast cancer
PS Claim 9; Page 94; 130pp; English.
PT This polypeptide sequence comprises the light chain variable region
CC (VL) of monoclonal anti-idiotype antibody 11D10 produced by
CC hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
CC naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype
CC response. It elicits an immune response against a specific epitope
CC of a high mol.wt. mucin of human milk fat globule (HMFG). It
CC induces an immunological response to HMFG in mice, rabbits, monkeys
CC and patients with advanced HMFG-associated tumours. Pharmaceutical
CC compositions and vaccines comprising 11D10, 11D10 polypeptides
CC and/or 11D10 polynucleotides (see also T85149-50) are claimed.
CC Also claimed are diagnostic kits and methods of using 11D10, 11D10
CC polypeptides and/or 11D10 polynucleotides, including methods of
CC treating HMFG-associated tumours. 11D10 is also used in a claimed
CC method of palliating HMFG-associated disease and in claimed kits to
CC detect or quantify anti-HMFG antibody.
SQ Sequence 145 AA;

Query Match   100.0%; Score 68; DB 25; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.06e+01;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   99 esedfvay 107
        |||||||||
Db   99 ESEDFVAY 107

RESULT 2
ID R80078 standard; Protein; 90 AA.
AC R80078;
DT 22-MAY-1996 (first entry)
DE Mouse derived light chain RT3 phage antibody pattern A.
KW Light chain; RT3; murine; catalytic antibody; bacteriophage;
KW pattern A.
OS Mus musculus.
FH Key   Location/Qualifiers
FT region 1..15
FT   /note= "framework region 1"
FT region 16..26
FT   /note= "complementarity determining region 1"
FT region 27..40
FT   /note= "framework region 2"
FT region 41..47
FT   /note= "complementarity determining region 2"
FT region 48..78
FT   /note= "framework region 3"
FT region 79..88
FT   /note= "complementarity determining region 3"
FT region 89..90
FT   /note= "framework region 4"
PN WO9527045-A1.
PD 12-OCT-1995.
PF 30-MAR-1994; 1995.
PR 30-MAR-1994; WO-U03420.
PA (IGEN-) IGEN INC.
PI Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;
DR WPI; 95-358624/46.
N-PSDB; T04625.
PT Production of catalytic antibodies displayed on phage - by
PT generating a gene library of antibody-derived domains and expressing
PT it in phage vectors
PS Disclosure; Fig 9; 133pp; English.
PT T04625 encodes R80078 mouse derived light chain RT3 phage antibody.
CC The DNA was used in the prepn. of catalytic antibody (CA) producing
CC bacteriophage. The CAs can be used to activate/deactivate a
CC biological function in an animal by enhancing the rate of cleavage,

CC or formation of a specific bond within a mol. in vivo.
SQ Sequence 90 AA;

Query Match   94.1%; Score 64; DB 16; Length 90;
Best Local Similarity 88.9%; Pred. No. 2.34e+01;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   99 esedfvay 77
        ||||||| ||
Db   99 ESEDFVAY 107

RESULT 3
ID R78972 standard; Protein; 107 AA.
AC R78972;
DT 21-DEC-1995 (first entry)
DE Light chain variable region for monoclonal antibody 5B6.
KW Monoclonal antibody; heavy metal; mercury; variable region;
KW light chain.
OS Synthetic.
PN WO9520607-A.
PD 03-AUG-1995.
PF 27-JAN-1995; U01199.
PR 27-JAN-1994; US-187407.
PA (BION-) BIONEBRASKA INC.
PI Lopez O, Wagner FW, Wylie DE;
WPI; 95-275415/36.
N-PSDB; Q97510.
PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
PS Claim 23; Page 70; 106pp; English.
CC Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate
CC covalent compound which was covalently bound to keyhole limpet
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC 5B6 and 3E8) were producing MAbs that were strongly positive
CC against glutathione-mercuric ions but negative against glutathione
CC without mercuric ions. RNA was isolated from hybridoma cells with
CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC were complementary to the 5' end of the CH1 domain of the heavy
CC chain expressed by the hybridoma of interest, or to the 5' and of
CC the C kappa domain. Some of the primers used for cDNA synthesis are
CC shown in Q97511-Q97518. The primer used for cDNA synthesis of the
CC variable region of a particular antibody polypeptide was also used
CC for PCR amplification of that variable region, in conjunction with
CC an appropriate V-region primer. In addition, the VH primer Q97518
CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences
CC of the PCR amplified nucleotides and the deduced AA sequences are given
CC in Q97498-Q97510 and the deduced AA sequences in R79241-R79250 &
CC R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are
CC used here.
SQ Sequence 107 AA;

Query Match   94.1%; Score 64; DB 14; Length 107;
Best Local Similarity 88.9%; Pred. No. 2.34e+01;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   99 esedfvay 107
        ||||||| ||
Db   99 ESEDFVAY 107

RESULT 4
ID R79247 standard; Protein; 107 AA.
AC R79247;
DT 21-DEC-1995 (first entry)
DE Light chain variable region for monoclonal antibody 1F10.
KW Monoclonal antibody; heavy metal; mercury; variable region;

```
KW   light chain.
OS   Synthetic.
PN   WO9520607-A.
PD   03-AUG-1995.
AC   U01199.
PF   27-JAN-1994; US-187407.
PR   27-JAN-1995; U01199.
PA   (BION-) BIONEBRASKA INC.
PI   Lopez O, Wagner FW, Wylie DE;
DR   N-PSDB; Q97504.
DR   WPI; 95-275415/36.
PT   New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT   monoclonal antibodies, used for detecting, removing, adding or
PT   neutralising heavy metals
PS   Claim 23; Page 62; 106pp; English.
CC   Hybridoma antibodies have been produced with the spleen cells of
CC   BALB/c mouse that had received multiple injections of mercuric ions
CC   reacted with glutathione to produce a mercuric ion coordinate
CC   covalent compound which was covalently bound to keyhole limpet
CC   hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC   5B6 and 3E8) were producing MAbs that were strongly positive
CC   against glutathione-mercuric ions but negative against glutathione
CC   without mercuric ions. RNA was isolated from hybridoma cells with
CC   guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC   by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC   were complementary to the 5' end of the CH1 domain of the heavy
CC   chain expressed by the hybridoma of interest, or to the 5' and of
CC   the C kappa domain. Some of the primers used for cDNA synthesis are
CC   shown in Q97511-Q97518. The primer used for cDNA synthesis of the
CC   variable region of a particular antibody polypeptide was also used
CC   for PCR amplification of that variable region, in conjunction with
CC   an appropriate V-region primer. In addition, the VH primer Q97518
CC   was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC   of the PCR amplified nucleotides were determined. These are given
CC   in Q97498-Q97510 and the deduced AA sequences in R79241-R79250 &
CC   R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC   and in the claims are different from the descriptions in the
CC   sequence listings. The descriptions in the sequence listings are
CC   used here.
SQ   Sequence 107 AA;

Query Match             94.1%;  Score 64;  DB 14;  Length 107;
Best Local Similarity   88.9%;
Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Db         79 esedfvydy 87
              ||||||| ||
Qy         99 ESEDFVAYY 107


RESULT 5

ID   R79250 standard; Protein; 107 AA.
AC   R79250;
DT   21-DEC-1995 (first entry)
DE   Light chain variable region for monoclonal antibody 5G4.
KW   Monoclonal antibody; heavy metal; mercury; variable region;
KW   light chain.
OS   Synthetic.
PN   WO9520607-A.
PD   03-AUG-1995.
AC   U01199.
PF   27-JAN-1994; US-187407.
PR   27-JAN-1994; U01199.
PA   (BION-) BIONEBRASKA INC.
PI   Lopez O, Wagner FW, Wylie DE;
DR   WPI; 95-275415/36.
DR   N-PSDB; Q97507.
PT   New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT   monoclonal antibodies, used for detecting, removing, adding or
PT   neutralising heavy metals
PS   Claim 23; Page 66; 106pp; English.
CC   Hybridoma antibodies have been produced with the spleen cells of
CC   BALB/c mouse that had received multiple injections of mercuric ions
CC   reacted with glutathione to produce a mercuric ion coordinate
CC   covalent compound which was covalently bound to keyhole limpet
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CC   hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC   5B6 and 3E8) were producing MAbs that were strongly positive
CC   against glutathione-mercuric ions but negative against glutathione
CC   without mercuric ions. RNA was isolated from hybridoma cells with
CC   guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC   by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC   were complementary to the 5' end of the CH1 domain of the heavy
CC   chain expressed by the hybridoma of interest, or to the 5' and of
CC   the C kappa domain. Some of the primers used for cDNA synthesis are
CC   shown in Q97511-Q97518. The primer used for cDNA synthesis of the
CC   variable region of a particular antibody polypeptide was also used
CC   for PCR amplification of that variable region, in conjunction with
CC   an appropriate V-region primer. In addition, the VH primer Q97518
CC   was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC   of the PCR amplified nucleotides were determined. These are given
CC   in Q97498-Q97510 and the deduced AA sequences in R79241-R79250 &
CC   R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC   and in the claims are different from the descriptions in the
CC   sequence listings. The descriptions in the sequence listings are
CC   used here.
SQ   Sequence 107 AA;

Query Match             94.1%;  Score 64;  DB 14;  Length 107;
Best Local Similarity   88.9%;
Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Db         79 esedfvydy 87
              ||||||| ||
Qy         99 ESEDFVAYY 107


RESULT 6

ID   R21310 standard; Protein; 108 AA.
AC   R21310;
DT   21-MAY-1992 (first entry)
DE   Light chain of Mlf clone.
KW   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW   plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW   specific binding pairs; replicable genetic display package.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   region          25..34
FT                   /label= CDR1
FT   region          50..56
FT                   /label= CDR2
FT   region          89..96
FT                   /label= CDR3
PN   WO9201047-A.
PD   23-JAN-1992.
PF   10-JUL-1991; G01134.
PR   10-JUL-1990; GB-015198.
PR   19-OCT-1990; GB-022845.
PR   12-NOV-1990; GB-024503.
PR   06-MAR-1991; GB-004744.
PR   15-MAY-1991; GB-010549.
PA   (CAMB-) CAMBRIDGE ANTIBODY.
PA   (MEDI-) MED RES COUNCIL.
PI   McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI   Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI   Winter GP, Bonnert TP;
DR   WPI; 92-058862/07.
PS   Example 46; Fig 52; 109pp; English.
PT   Producing members of specific binding pairs - by expression in
PT   recombinant host cells with a secreting replicable genetic
PT   display package.
CC   The sequence is the light chain of clone Mlf encoding an scFv frag-
CC   ment specific for both hen and turkey egg lysozyme (HEL and TEL).
CC   The DNA encoding the chain was amplified from a cDNA library prepd.
CC   from the spleen of an unimmunised mouse. The corresponding heavy
CC   chain was also amplified from an existing construct, pSW1-VHD1.3
CC   (Ward et al. 1989). The two fragments were assembled via a linker
CC   to prepare an scFv construct which was ligated into the fdCAT2
CC   vector for expression on the surface of fd bacteriophage. In this
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CC   way, the VL domain was replaced by a library of VL domains to allow
CC   for selection of a broader range of antibody specificities. Several
CC   clones were isolated which bound to TEL (the parent antibody D1.3
CC   binds exclusively to HEL). The sequences of the light chains of
CC   two of these clones, MF1 and M21 are given in R21310 and R21311
CC   respectively. The D1.3 light chain is given in R21309.
CC   See also R21260-307, 309-312, R22450, R22555, R22567-81.
SQ   Sequence  108 AA;

Qy   79 esedfvdy 87
        ||||||| ||
Db   99 ESEDFVAY 107

Query Match      94.1%;  Score 64;  DB 4;  Length 108;
Best Local Similarity   88.9%;  Pred. No. 2.34e+01;
Matches   8;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;
```

```
● RESULT 7
ID   P30251 standard; peptide; 146 AA.
AC   P30251;
DT   25-MAY-1992 (first entry)
DE   Sequence of the leader, variable region and first 16 AAs of
DE   the constant region of the kappa-chain (light chain) of MOPC41.
KW   Diagnosis; therapy; Immunoglobulin.
OS   Homo sapiens.
FH   Key            Location/Qualifiers
FT   region         1..22
FT                  /label= leader
FT   region         23..130
FT                  /label= variable
FT   region         131..146
FT                  /label= constant
PN   EP-88994-A.
PD   21-SEP-1983.
PF   10-MAR-1983; 001655.
PR   15-MAR-1982; US-358414.
PR   05-DEC-1983; US-558551.
PA   (SCHE ) SCHERING CORP.
PA   (DNAX-) DNAX RES INST.
PI   Moore KW, Zaffaroni A;
DR   WPI; 83-77290/39.
DR   N-PSDB; N30165.
PT   Transformed expression vectors or plasmid(s) - with double
PT   stranded DNA sequence coding only for desired part of polypeptide
PT   chain
PT   Example: Page 40-41; 68pp; English.
PT   The pref. vector or plasmid of the invention has a double-stranded
PT   DNA seq. coding for a variable region of a light or heavy chain of
PT   IgG, or for a variable region of a light or heavy chain of an
PT   immunoglobulin specific for an enzyme or surface protein. The
PT   sequence esp. codes for a variable region of a light chain having 95-
PT   115 AAs or for a variable region of a heavy chain having 110-125 AAs
PT   esp. including the D region of the heavy chain.
SQ   Sequence  146 AA;

Query Match      94.1%;  Score 64;  DB 4;  Length 146;
Best Local Similarity   88.9%;  Pred. No. 2.34e+01;
Matches   8;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy   101 esedfvdy 109
         |||||| ||
Db   99 ESEDFVAY 107
```

```
RESULT 8
ID   W02280 standard; Protein; 243 AA.
AC   W02280;
DT   29-OCT-1996 (first entry)
DE   52C9 anti-c-erbB-2 two single chain Fv construct.
KW   52C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sFv;
KW   construct; polypeptide linker; C-terminal amino acid sequence;
KW   in vivo imaging; drug targetting experiment; homodimer;
KW   increased; binding avidity; tissue retention time.
OS   Homo sapiens.
FH   Key            Location/Qualifiers
KW   Peptide        118..133
FT                  /label= linker
PN   US5534254-A.
PN   09-JUL-1996; 831967.
PF   06-FEB-1992; 831967.
PR   06-FEB-1992; US-831967.
PR   07-OCT-1993; US-133804.
PA   (CHIR ) CHIRON CORP.
PA   (CREA-) CREATIVE BIOMOLECULES INC.
PI   Huston JS, Oppermann H, Ring DB;
DR   WPI; 96-333194/33.
DR   N-PSDB; T36880.
PT   Compsns. contg. antigen-targetting antibody fragment constructs -
PT   comprising dimer of single-chain Fv fragments
PS   Example 1; Columns 33-36; 30pp; English.
CC   Variable heavy (VH) and variable light (VL) genes were cloned from
CC   a 52C9 hybridoma cDNA library, using probes directed toward the
CC   antibody constant and joining regions. A two single chain Fv (sFv)
CC   gene was constructed by connecting the VH and VL genes with a
CC   Ser rich polypeptide linker. The resulting 52C9 two sFv gene,
CC   which encodes the present sequence, was inserted into an expression
CC   vector, transformed into E. coli, and protein expression induced by
CC   the addn. of IPTG to the culture medium.
CC   A compsn. comprising a carrier and the 2 sFv protein prod. can be
CC   used for in vivo imaging, and drug targetting experiments. The
CC   2 sFv protein prod. is a homodimer, in which both fragments target
CC   the same antigen, therefore giving greater binding avidity and
CC   longer tissue retention times, compared to individual sFv protein
CC   prod. fragments.
SQ   Sequence  243 AA;

Query Match      94.1%;  Score 64;  DB 18;  Length 243;
Best Local Similarity   88.9%;  Pred. No. 2.34e+01;
Matches   8;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy   212 esedfvyy 220
         |||||| ||
Db   99 ESEDFVAY 107
```

```
RESULT 9
ID   R39569 standard; Protein; 246 AA.
AC   R39569;
DT   07-FEB-1994 (first entry)
DE   Sequence of 52C9 sFv protein.
KW   single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;
OS   Synthetic.
PN   WO9316185-A.
PN   19-AUG-1993; U01055.
PF   05-FEB-1993; US-831967.
PR   06-FEB-1992; US-831967.
PA   (CEMU ) CETUS ONCOLOGY CORP.
PA   (CREA-) CREATIVE BIOMOLECULES INC.
PI   Huston JS, Oppermann H, Ring DB;
DR   WPI; 93-272889/34.
DR   N-PSDB; Q46084.
PT   New single chain Fv polypeptide binding to C-erbB-2 tumour
PT   antigen - for imaging or treating breast or ovarian cancer etc.
PS   Claim 4; pages 60-61; 87pp; English.
CC   c-erbB-2 refers to a protein antigen expressed on the surface of
CC   tumour cells, such as breast and ovarian tumour cells, which is an
CC   approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric
CC   pt. of about 5.3 (see Q46083, R39568). A single chain Fv (sFv)
CC   is a covalently linked VH-VL heterodimer which is expressed from
CC   a gene fusion including genes connected by
CC   a peptide-encoding linker. Such linker sequences are set forth in
CC   AA residues 116-135 in R39569, which includes part of the 16 AA
CC   linker sequences in R39572. Using Q46084 for the 52C9 monoclonal
CC   antibody, a single chain polypeptide can be produced having a
```

Column 1

```
CC   binding affinity for a c-erbB-2 related antigen. 'X' in R39569
CC   refers to the location of a stop codon in Q46084.
SQ   Sequence 246 AA;

     Query Match     94.1%;  Score 64;  DB 8;  Length 246;
     Best Local Similarity   88.9%;
     Matches   8;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   99 ESEDFVAYY 107

Db  212 esedfvyy 220
          ||||||| ||
Qy   99 ESEDFVAYY 107

RESULT 10
ID   R39571 standard; Protein; 534 AA.
AC   R39571;
DT   07-FEB-1994 (first entry)
DR   N-PSDB: Q46086.
DR   WPI: 93-272889/34.
PI   Houston LL, Huston JS, Oppermann H, Ring DB;
PA   (CETU ) CETUS ONCOLOGY CORP.
PA   (CREA-) CREATIVE BIOMOLECULES INC.
PR   06-FEB-1992; US-831967.
PR   05-FEB-1993; U01055.
PD   19-AUG-1993.
PF   WO9316185-A.
DE   Synthetic.
DE   Tumour antigen; c-erbB-2; G-FIT.
PS   Sequence of G-FIT.
PT   New single chain Fv polypeptide binding to c-erbB-2 tumour
PT   antigen - for imaging or treating breast or ovarian cancer etc.
CC   Example; pages 65-68; 87pp; English.
CC   c-erbB-2 refers to a protein antigen expressed on the surface of
CC   tumour cells, such as breast and ovarian tumour cells, which is an
CC   approx. 200.000 mol. wt. acidic glycoprotein having an isoelectric
CC   pt. of about 5.3 (see Q46083, R39568).
SQ   Sequence 534 AA;

     Query Match     94.1%;  Score 64;  DB 8;  Length 534;
     Best Local Similarity   88.9%;
     Matches   8;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Db  503 esedfvyy 511
          ||||||| ||
Qy   99 ESEDFVAYY 107

RESULT 11
AC   R92829;
     R92829 standard; Protein; 255 AA.
DT   09-MAY-1996 (first entry)
DR   N-PSDB: T04179.
DR   WPI: 95-338286/44.
PI   Atsushi O, Hirofumi Y, Ikunoshin K, Takashi T, Yoshinobu O;
PA   (TAKI ) TAKARA SHUZO CO LTD.
PR   30-MAR-1994; JP-082693.
PR   14-MAR-1995; 301664.
PD   04-OCT-1995.
PN   EP-675199-A2.
FT   domain
FT        194..251
FT        /note="Fc binding domain-like structure"
FT   domain
FT        136..193
FT        /note="Fc binding domain-like structure"
FT   protein
FT        26..126
FT        /note="variable light chain"
FH   Key                  Location/Qualifiers
OS   Synthetic.
KW   haemagglutinin; variable light chain; therapy.
KW   Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis;
DE   C179Fv-PP variable light chain sequence.
PT   Gene encoding variable region of anti-human influenza A type virus
PT   antibody - useful for prodn. of artificial antibodies
PS   Example 4; Page 33-35; 42pp; English.
```

Column 2

```
CC   This sequence represents the variable light chain of C179Fv-PP. The
CC   variable heavy chain sequence of C179Fv-PP is shown in R92829. These
CC   sequences form an anti-human influenza A type virus antibody. The
CC   antibody recognises the stem region of the haemagglutinin (HA) molecule
CC   of the H1N1 and H2N2 subtypes of human influenza A type virus, and shows
CC   neutralisation activity against these two subtypes. The antibody shows
CC   no recognition of the H3N2 subtype. This sequence and the variable light
CC   chain coding sequence (see T04160) are useful in the production of
CC   artificial antibodies and antigen-binding polypeptides. These artificial
CC   antibodies and polypeptides are useful in the diagnosis and treatment of
CC   human influenza. As the antibodies recognise the stem region of the HA
CC   molecule, the influenza virus will be recognised even if the HA molecule
CC   changes. This provides an advantage over current vaccines, as the virus
CC   periodically alters it's HA molecule.
SQ   Sequence 255 AA;

     Query Match     89.7%;  Score 61;  DB 16;  Length 255;
     Best Local Similarity   66.7%;
     Matches   6;  Conservative  3;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   99 ESEDFVAYY 107

Db  101 qaedfvysy 109
          :||||:||
Qy   99 ESEDFVAYY 107

RESULT 12
ID   R82835 standard; Protein; 392 AA.
AC   R82835;
DT   09-MAY-1996 (first entry)
DE   scFv-PP.
KW   Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis;
KW   haemagglutinin; variable heavy chain; therapy.
OS   Synthetic.
FH   Key                  Location/Qualifiers
FT   protein
FT        23..144
FT        /note="variable heavy chain"
FT   protein
FT        164..263
FT        /note="variable light chain"
FT   domain
FT        273..330
FT        /note="Fc binding domain-like structure"
FT   domain
FT        331..388
FT        /note="Fc binding domain-like structure"
PN   EP-675199-A2.
PD   04-OCT-1995.
PR   14-MAR-1995; 301664.
PR   30-MAR-1994; JP-082693.
PA   (TAKI ) TAKARA SHUZO CO LTD.
PI   Atsushi O, Hirofumi Y, Ikunoshin K, Takashi T, Yoshinobu O;
DR   WPI: 95-338286/44.
DR   N-PSDB: T04180.
PT   Gene encoding variable region of anti-human influenza A type virus
PT   antibody - useful for prodn. of artificial antibodies
PS   Example 4; Page 36-38; 42pp; English.
CC   This sequence represents the scFv-PP fusion polypeptide. This sequence
CC   is an anti-human influenza A type virus antibody. The antibody
CC   recognises the stem region of the haemagglutinin (HA) molecule of the
CC   H1N1 and H2N2 subtypes of human influenza A type virus, and shows
CC   neutralisation activity against these two subtypes. The antibody shows
CC   no recognition of the H3N2 subtype. Artificial antibodies (such as this)
CC   and polypeptides are useful in the diagnosis and treatment of human
CC   influenza. As the antibodies recognise the stem region of the HA
CC   molecule, the influenza virus will be recognised even if the HA molecule
CC   changes. This provides an advantage over current vaccines, as the virus
CC   periodically alters it's HA molecule.
SQ   Sequence 392 AA;

     Query Match     89.7%;  Score 61;  DB 16;  Length 392;
     Best Local Similarity   66.7%;
     Matches   6;  Conservative  3;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   99 ESEDFVAYY 107

Db  238 qaedfvsyy 246
          :||||:||
Qy   99 ESEDFVAYY 107
```

RESULT 13
```
ID   R82826 standard; Protein; 98 AA.
AC   R82826;
DT   08-MAY-1996 (first entry)
DE   Variable light region of the anti-human influenza A type virus antibody.
KW   Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis;
KW   haemagglutinin; variable heavy chain; therapy.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   region          28..33
FT                   /label= CDR1
FT   region          50..55
FT                   /label= CDR2
FT   region          90..94
FT                   /label= CDR3
PN   EP-675199-A2.
PD   04-OCT-1995.
PF   14-MAR-1995; 301664.
PR   30-MAR-1994; JP-082693.
PA   (TAKA ) TAKARA SHUZO CO LTD.
PI   Atsushi O, Hirofumi Y, Ikunoshin K, Takashi T, Yoshinobu O;
DR   WPI; 95-338286/44.
DR   N-PSDB; T04160.
PT   Gene encoding variable region of anti-human influenza A type virus
PT   antibody - useful for prodn. of artificial antibodies
PS   Claim 2; Page 20; 42pp; English.
CC   This sequence represents the variable heavy chain region of an anti-human
CC   influenza A type virus antibody. The antibody recognises the stem region
CC   of the haemagglutinin (HA) molecule of the H1N1 and H2N2 subtypes of
CC   human influenza A type virus, and shows neutralisation activity against
CC   these two subtypes. The antibody shows no recognition of the H3N2
CC   subtype. The DNA encoding this sequence and the variable heavy chain
CC   coding sequence (see T04159) are useful in the production of artificial
CC   antibodies and antigen-binding polypeptides. These artificial antibodies
CC   and polypeptides are useful in the diagnosis and treatment of human
CC   influenza. As the antibodies recognise the stem region of the HA
CC   molecule, the influenza virus will be recognised even if the HA
CC   molecule changes. This provides an advantage over current vaccines, as the virus
CC   periodically alters it's HA molecule.
SQ   Sequence 98 AA;

Query Match             85.3%;  Score 58;  DB 16;  Length 98;
Best Local Similarity   55.6%;  Pred. No. 7.56e+01;
Matches    5;  Conservative    4;  Mismatches   0;  Indels   0;  Gaps   0;

Qy         79 gaqdfvsy 87
              :::|||:||
           99 ESEDFVAY 107
```

RESULT 14
```
ID   R80079 standard; Protein; 90 AA.
AC   R80079;
DT   22-MAY-1996 (first entry)
DE   Mouse derived light chain RT3 phage antibody pattern C.
KW   Light chain; RT3; murine; catalytic antibody; bacteriophage;
KW   pattern C.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   region          1..15
FT                   /note= "framework region 1"
FT   region          16..26
FT                   /note= "complementarity determining region 1"
FT   region          27..40
FT                   /note= "framework region 2"
FT   region          41..47
FT                   /note= "complementarity determining region 2"
FT   region          48..78
FT                   /note= "framework region 3"
FT   region          79..88
FT                   /note= "complementarity determining region 3"
FT   region          89..90
FT                   /note= "framework region 4
FT                   N-terminal fragment"
PN   WO9527045-A1.
PD   12-OCT-1995.
PF   30-MAR-1994; U03420.
PR   30-MAR-1994; WO-U03420.
PA   (IGEN-) IGEN INC.
PI   Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI   Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;
DR   WPI; 95-358624/46.
DR   N-PSDB; T04626.
PT   Production of catalytic antibodies displayed on phage - by
PT   generating a gene library of antibody-derived domains and expressing
PT   it in phage vectors
PS   Disclosure; Fig 9; 133pp; English.
CC   T04626 encodes R80079 mouse derived light chain RT3 phage antibody.
CC   The DNA was used in the prepn. of catalytic antibody (CA) producing
CC   bacteriophage. The CAs can be used to activate/deactivate a
CC   biological function in an animal by enhancing the rate of cleavage,
CC   or formation of a specific bond within a mol. in vivo.
SQ   Sequence 90 AA;

Query Match             83.8%;  Score 57;  DB 16;  Length 90;
Best Local Similarity   77.8%;  Pred. No. 9.17e+01;
Matches    7;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db         69 esedfadyy 77
              ||||| ||
Qy         99 ESEDFVAYY 107
```

RESULT 15
```
ID   W31726 standard; Peptide; 107 AA.
AC   W31726;
DT   29-APR-1998 (first entry)
DE   Alpha light chain amino acid sequence of the Fab molecule clone L1.
KW   Alpha light chain; Fab molecule; binding; hepatitis C virus; HCV;
KW   E2 antigen; combinatorial antibody library; vaccine; antibody;
KW   recombinant human monoclonal antibody; immunological binding affinity;
KW   passive immunity.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Region          23..34
FT                   /note= "CDR 1"
FT   Region          50..56
FT                   /note= "CDR 2"
FT   Region          89..97
FT                   /note= "CDR 3"
PN   WO9740176-A1.
PD   30-OCT-1997.
PF   18-APR-1997; E01977.
PR   17-APR-1997; US-844215.
PR   19-APR-1996; US-635109.
PA   (ALLA/) ALLANDER T E.
PA   (PERS/) PERSSON M A.
PI   Allander TE, Persson MA;
DR   WPI; 97-535857/49.
DR   N-PSDB; T08837.
PT   New human monoclonal antibodies to hepatitis C virus E2 antigen -
PT   obtained using a combinatorial antibody library prepared using RNA
PT   from a HCV infected subject, useful for vaccine preparation
PS   Claim 5; Fig 2E; 103pp; English.
CC   The present sequence represents the alpha light chain peptide sequence
CC   of the Fab molecule, clone L1. This immunoglobulin molecule is
CC   capable of specifically binding with the hepatitis C virus (HCV)
CC   E2 antigen. The present sequence was obtained from a combinatorial
CC   antibody library. The alpha light chain peptide can be used to construct
CC   a recombinant human monoclonal antibody (MAb). The monoclonal antibodies
CC   exhibit immunological binding affinity for HCV E2 antigen and are
CC   cross-reactive with different HCV strains. They can be used to produce
CC   vaccine compositions which can be used to provide antibodies to HCV in
CC   a subject or to provide passive immunity or to treat HCV infected
```

CC   subjects. They can also be used to detect HCV and to monitor anti-HCV
CC   therapeutic treatment.
CC   note: this sequence is allegedly encoded by T88837; however, the
CC   peptide encoded by that nucleotide sequence differs considerably to the
CC   present peptide.
SQ   Sequence   107 AA;

Query Match   83.8%;   Score 57;   DB 28;   Length 107;
Best Local Similarity   77.8%;   Pred. No. 9.17e+01;
Matches   7;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Db   79 esedfavyy 87
              ||||| ||
Qy   99 ESEDFVAYY 107

Search completed: Tue Apr 20 14:01:59 1999
Job time : 16 secs.

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MPSRCH (TM)

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

● on on: Tue Apr 20 14:01:07 1999; MasPar time 3.31 seconds
           ----101.886 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-836-455-2
                (99-107) from US08836455.pep (3 of 3)
Perfect Score: 68
Sequence: 1 ESEDFVAY 9

Scoring table: PAM 150
                Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: pir58
                1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 25.001; Variance 40.079; scale 0.624

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Match	Length	DB	ID	Description	Pred. No.
1	64	94.1	88	2	PL0261	Ig kappa chain V regi	4.48e-01
2	64	94.1	106	2	PL0260	Ig kappa chain V regi	4.48e-01
3	64	94.1	106	2	PL0259	Ig kappa chain V regi	4.48e-01
4	64	94.1	130	1	KVMSM4	Ig kappa chain precur	4.48e-01
5	61	89.7	103	2	H30502	Ig kappa chain V regi	4.48e-01
6	61	89.7	109	2	F30607	Ig kappa chain V-III	1.48e+00
7	58	85.3	92	2	S37510	Ig kappa chain V regi	4.74e+00
8	57	83.8	91	2	S17622	Ig kappa chain V regi	6.94e+00
9	57	83.8	98	2	PH1062	Ig light chain V regi	6.94e+00
10	57	83.8	101	2	B28840	Ig kappa chain V regi	6.94e+00
11	57	83.8	106	2	PL0262	Ig kappa chain V regi	6.94e+00
12	57	83.8	108	4	B47271	nitrophenyl phosphona	6.94e+00
13	57	83.8	117	1	KVMS3B	Ig kappa chain precur	6.94e+00
14	57	83.8	129	2	D32513	Ig kappa chain V regi	6.94e+00
15	56	82.4	82	2	S34090	Ig kappa chain V regi	1.01e+01
16	56	82.4	88	2	S21524	Ig kappa chain V regi	1.01e+01
17	56	82.4	117	2	S41812	Ig kappa chain variab	1.01e+01
18	56	82.4	128	2	S46372	IG light chain V regi	1.01e+01
19	56	82.4	132	2	S38646	Ig kappa chain V regi	1.01e+01
20	56	82.4	236	2	S75373	probable DNA-(apurini	1.01e+01
21	56	82.4	613	1	Q0BE33	BBRF1 protein - human	1.01e+01
22	55	80.9	54	1	JT0521	Ig kappa chain V-III	1.47e+01
23	55	80.9	120	2	S21667	Ig kappa chain V regi	1.47e+01
24	55	80.9	125	2	S04936	Ig kappa chain precur	1.47e+01
25	55	80.9	130	2	PL0113	Ig kappa chain precur	1.47e+01
26	55	80.9	764	2	S14113	1-phosphatidylinosito	1.47e+01
27	54	79.4	86	2	S34099	Ig kappa chain V-III	2.12e+01
28	54	79.4	86	2	S16833	Ig kappa chain V regi	2.12e+01
29	54	79.4	91	2	S16837	Ig kappa chain V-III	2.12e+01
30	54	79.4	92	2	S37520	Ig kappa chain V regi	2.12e+01
31	54	79.4	92	2	S37507	Ig kappa chain V regi	2.12e+01
32	54	79.4	92	2	S37523	Ig kappa chain V regi	2.12e+01
33	54	79.4	92	2	S37502	Ig kappa chain V regi	2.12e+01
34	54	79.4	92	2	S37518	Ig kappa chain V regi	2.12e+01
35	54	79.4	92	2	S37514	Ig kappa chain V regi	2.12e+01
36	54	79.4	92	2	S37503	Ig kappa chain V regi	2.12e+01
37	54	79.4	92	2	S37512	Ig kappa chain V regi	2.12e+01
38	54	79.4	92	2	S37513	Ig kappa chain V regi	2.12e+01
39	54	79.4	93	2	S37526	Ig kappa chain V regi	2.12e+01
40	54	79.4	93	2	S37528	Ig kappa chain V regi	2.12e+01
41	54	79.4	93	2	S37508	Ig kappa chain V regi	2.12e+01
42	54	79.4	107	2	S34005	Ig kappa chain V-III	2.12e+01
43	54	79.4	110	2	E30607	Ig kappa chain V-III	2.12e+01
44	54	79.4	128	2	S40379	Ig kappa chain V-J re	2.12e+01
45	54	79.4	144	2	PL0106	Ig kappa chain precur	2.12e+01

ALIGNMENTS

RESULT   1

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ENTRY          PL0261    #type fragment
TITLE          Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
               09-May-1997
ACCESSIONS     PL0261
REFERENCE      PL0231
  #authors     Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
               D.; Marshak-Rothstein, A.; Weigert, M.
  #journal     J. Exp. Med. (1990) 171:265-297
  #title       Anti-DNA antibodies from autoimmune mice arise by clonal
               expansion and somatic mutation.
  #cross-references MUID:90111618
  #accession   PL0261
  ##molecule_type mRNA
  ##residues   1-88 ##label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE
          1-5      #region framework 1\
          6-16     #region complementarity-determining 1\
          17-31    #region framework 2\
          32-38    #region complementarity-determining 2\
          39-70    #region framework 3\
          71-79    #region complementarity-determining 3\
          80-88    #region framework 4
SUMMARY   #length 88  #checksum 7092

          Query Match     94.1%;   Score 64;  DB 2;  Length 88;
          Best Local Similarity  88.9%;  Pred. No. 4.48e-01;
          Matches   8;  Conservative   0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    99 ESEDFVAY 107
         |||||| ||
Db    61 ESEDFVDYY 69
```

RESULT   2

```
ENTRY          PL0260    #type fragment
TITLE          Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           16-Aug-1996 #sequence_revision 16-Sep-1992 #text_change
ACCESSIONS     PL0260
REFERENCE      PL0231
  #authors     Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
```

Left column

```
#journal    J. Exp. Med. (1990) 171:265-297
#title      Anti-DNA antibodies from autoimmune mice arise by clonal
            expansion and somatic mutation.
#cross-references MUID:90111618
#accession  PI0260
            ##molecule_type mRNA
#residues   1-106 ##label SHL
KEYWORDS    #superfamily immunoglobulin V region; immunoglobulin homology
CLASSIFICATION  heterotetramer; immunoglobulin
FEATURE
 1-23       #region framework 1\
 24-34      #region complementarity-determining 1\
 35-49      #region framework 2\
 50-56      #region complementarity-determining 2\
 57-88      #region framework 3\
 89-97      #region complementarity-determining 3\
 98-106     #region framework 4
SUMMARY     #length 106 #checksum 2157

Qy   99 ESEDFVAYY 107
        |||||| ||
Db   79 ESEDFVDYY 87

Query Match     94.1%;   Score 64;   DB 2;   Length 106;
Best Local Similarity   88.9%;   Pred. No. 4.48e-01;
Matches     8;   Conservative    0;   Mismatches    1;   Indels   0;   Gaps   0;

RESULT 3
ENTRY       PI0259     #type fragment
TITLE       Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
ORGANISM    #formal_name Mus musculus #common_name house mouse
DATE        16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
REFERENCE   PI0259
            PI0231
 #authors   Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
            D.; Marshak-Rothstein, A.; Weigert, M.
 #journal   J. Exp. Med. (1990) 171:265-297
 #title     Anti-DNA antibodies from autoimmune mice arise by clonal
            expansion and somatic mutation.
 #cross-references MUID:90111618
 #accession PI0259
            ##molecule_type mRNA
 #residues  1-106 ##label SHL
KEYWORDS    #superfamily immunoglobulin V region; immunoglobulin homology
CLASSIFICATION  heterotetramer; immunoglobulin
FEATURE
 1-23       #region framework 1\
 24-34      #region complementarity-determining 1\
 35-49      #region framework 2\
 50-56      #region complementarity-determining 2\
 57-88      #region framework 3\
 89-97      #region complementarity-determining 3\
 98-106     #region framework 4
SUMMARY     #length 106 #checksum 2162

Qy   99 ESEDFVAYY 107
        |||||| ||
Db   79 ESEDFVDYY 87

Query Match     94.1%;   Score 64;   DB 2;   Length 106;
Best Local Similarity   88.9%;   Pred. No. 4.48e-01;
Matches     8;   Conservative    0;   Mismatches    1;   Indels   0;   Gaps   0;

RESULT 4
ENTRY       KVMSM4     #type complete
TITLE       Ig kappa chain precursor V region (MOPC 41) - mouse
ORGANISM    #formal_name Mus musculus #common_name house mouse
DATE        24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change
```

Right column

```
ACCESSIONS  A93211; B93211; A93815; A94239; A01922; A01923
REFERENCE   16-Aug-1996
 #authors   Seldman, J.G.; Max, E.E.; Leder, P.
 #journal   Nature (1979) 280:370-375
 #title     A kappa-immunoglobulin gene is formed by site-specific
            recombination without further somatic mutation.
 #cross-references MUID:79221900
 #accession A93211
            ##molecule_type DNA
 #residues  1-130 ##label PC41
 #note      the sequences were determined from the differentiated
            gene MOPC 41 and the germline gene VK41
REFERENCE   A93815
 #authors   Burstein, Y.; Schechter, I.
 #journal   Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720
 #title     Amino acid sequence of the NH-2-terminal extra piece segments
            of the precursors of mouse immunoglobulin lambda-1-type and
            kappa-type light chains.
 #cross-references MUID:77148916
 #accession A93815
            ##molecule_type protein
 #residues  1-33 ##label BUR
 #note      Met-3 is apparently used as an alternative initiator in
            25% of the chains
REFERENCE   A94239
 #authors   Gray, W.R.; Dreyer, W.J.; Hood, L.
 #journal   Science (1967) 155:465-467
 #title     Mechanism of antibody synthesis: size differences between
            mouse kappa chains.
 #cross-references MUID:67056897
 #accession A94239
            ##molecule_type protein
 #residues  23-49,'B',51-53,'LSB',57-58,'ZZ',61-62,'B2',65-76,'B',
            78-108,110-130 ##label GRA
            ##experimental_source Bence Jones protein MOPC 41
GENETICS
 #introns   19/1
COMPLEX     An immunoglobulin heterotetramer subunit consists of two
            identical light (kappa or lambda) and two identical heavy
            (alpha, delta, epsilon, gamma, or mu) chains usually
            stabilized by interchain disulfide bonds. In some cases,
            such as IgA and IgM, the subunits associate into larger
            oligomers.
KEYWORDS    #superfamily immunoglobulin V region; immunoglobulin homology
CLASSIFICATION  alternative initiators; heterotetramer; immunoglobulin
FEATURE
 1-22       #domain signal sequence #status experimental #label
 3-22           SIG1\
                #domain signal sequence #status experimental #label
 23-130         SIG2\
                #product Ig kappa chain V region (MOPC 41) #status
                experimental #label M41\
 38-112         #domain immunoglobulin homology #label M41\
 45-110         #disulfide_bonds #status predicted
SUMMARY     #length 130 #molecular-weight 14311 #checksum 6707

Qy  101 ESEDFVDYY 109
        |||||| ||
Db   99 ESEDFVAYY 107

Query Match     94.1%;   Score 64;   DB 1;   Length 130;
Best Local Similarity   88.9%;   Pred. No. 4.48e-01;
Matches     8;   Conservative    0;   Mismatches    1;   Indels   0;   Gaps   0;

RESULT 5
ENTRY       H30502     #type complete
TITLE       Ig kappa chain V region (D42) - mouse
ORGANISM    #formal_name Mus musculus #common_name house mouse
```

DATE   03-Nov-1988 #sequence_revision 03-Aug-1992 #text_change
              20-Mar-1998
ACCESSIONS   H30502
REFERENCE   A30502
  #authors   Eilat, D.; Webster, D.M.; Rees, A.R.
  #journal   J. Immunol. (1988) 141:1745-1753
  #title   V region sequences of anti-DNA and anti-RNA autoantibodies
               from NZB/NZW F-1 mice.
  #cross-references MUID:88315787
  ##accession   H30502
  ##status   preliminary
  ##molecule_type mRNA
  ##residues   1-103
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY   #length 103 #molecular-weight 11280 #checksum 1572

Db   76 EPEDFVYYY 84
               |:||||| ||
Qy   99 ESEDFVAYY 107

Query Match   89.7%;   Score 61; DB 2; Length 103;
Best Local Similarity 77.8%;   Pred. No. 1.48e+00;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

RESULT   6
ENTRY   F30607   #type fragment
TITLE   Ig kappa chain V-III region (Bor) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change
              16-Aug-1996
ACCESSIONS   F30607
REFERENCE   A30601
  #authors   Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.;
               Fernandez, J.; Carson, D.; Solomon, A.; Mendez, E.;
               Frangione, B.
  #journal   J. Immunol. (1989) 142:3158-3163
  #title   Structural and idiotypic characterization of the L chains of
               human IgM autoantibodies with different specificities.
  #cross-references MUID:8921579
  ##accession   F30607
  ##status   preliminary
  ##molecule_type protein
  ##residues   1-109 ##label GON
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY   #length 109 #checksum 6514

Query Match   89.7%;   Score 61; DB 2; Length 109;
Best Local Similarity 77.8%;   Pred. No. 1.48e+00;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Db   80 EPEDFVVYY 88
               |:||||| ||
Qy   99 ESEDFVAYY 107

RESULT   7
ENTRY   S37510   #type fragment
TITLE   Ig kappa chain V region (V-kappa 3) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
              08-Sep-1997
ACCESSIONS   S37510
REFERENCE   S37501
  #authors   Klein, U.; Kueppers, R.; Rajewsky, K.
  #submission submitted to the EMBL Data Library, September 1993
  #description Human IgM(+)IgD(+) cells, the major B cell subset in the
               peripheral blood, expresses V(kappa) genes with no or
               little somatic mutation throughout life.
  #accession   S37510

ACCESSIONS   ##status   preliminary
              ##molecule_type mRNA
              ##residues   1-92 ##label KLE
              ##cross-references EMBL:226601; NID:g405662; PID:g405663
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY   #length 92 #checksum 6347

Query Match   85.3%;   Score 58; DB 2; Length 92;
Best Local Similarity 66.7%;   Pred. No. 4.74e+00;
Matches   6; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Db   63 QPEDFVYYY 71
               :|||| ||
Qy   99 ESEDFVAYY 107

RESULT   8
ENTRY   S17622   #type complete
TITLE   Ig kappa chain V region - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
              09-May-1997
ACCESSIONS   S17622
REFERENCE   S17230
  #authors   Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
  #journal   Nature (1991) 352:624-628
  #title   Making antibody fragments using phage display libraries.
  #cross-references MUID:91326098
  ##accession   S17622
  ##status   preliminary
  ##molecule_type nucleic acid
  ##residues   1-91 ##label CLA
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY   #length 91 #molecular-weight 9895 #checksum 3446

Query Match   83.8%;   Score 57; DB 2; Length 91;
Best Local Similarity 77.8%;   Pred. No. 6.94e+00;
Matches   7; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Db   71 ESEDFADYY 79
               |||||| ||
Qy   99 ESEDFVAYY 107

RESULT   9
ENTRY   PHI062   #type fragment
TITLE   Ig light chain V region (clone 202.105) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
              15-Jun-1996
ACCESSIONS   PHI062
REFERENCE   PH0971
  #authors   Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
  #journal   J. Exp. Med. (1992) 176:761-779
  #title   Both IgM and IgG anti-DNA antibodies are the products of
               clonally selective B cell stimulation in (NZB x NZW)F1
               mice.
  #accession   PHI062
              ##status   nucleic acid sequence not shown
              ##molecule_type mRNA
              ##residues   1-98 ##label TIL
              ##experimental_source B cell, strain [NZB x NZW]F1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   immunoglobulin
SUMMARY   #length 98 #checksum 6933

Query Match   83.8%;   Score 57; DB 2; Length 98;
Best Local Similarity 77.8%;   Pred. No. 6.94e+00;
Matches   7; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Db   79 ESEDFADYY 87

Qy   99 ESEDFVAYY 107

RESULT   10
ENTRY   B28840   #type fragment
TITLE   Ig kappa chain V region (HP27) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change
            16-Aug-1996
ACCESSIONS A91028
REFERENCE   B28840; I25114
  #authors Oller, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau,
            M.
  #journal EMBO J. (1985) 4:3681-3688
  #title   The idiotypic network and the internal image: possible
            regulation of a germ-line network by paucigene encoded Ab2
            (anti-idiotypic) antibodies in the GAT system.
  #cross-references MUID:86136012
  #accession B28840
            ##molecule_type mRNA
            ##residues 1-101 ##label OLL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY   #length 101 #checksum 7015

Db   73 ESEDFADY 81
           ||||| ||
Qy   99 ESEDFVAYY 107

Query Match   83.8%; Score 57; DB 2; Length 101;
Best Local Similarity   77.8%; Pred. No. 6.94e+00;
Matches   7; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

RESULT   11
ENTRY   PL0262   #type fragment
TITLE   Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   16-Aug-1996 #sequence_revision 16-Sep-1992 #text_change
            16-Aug-1996
ACCESSIONS PL0262
REFERENCE   PL0231
  #authors Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
            D.; Marshak-Rothstein, A.; Weigert, M.
  #journal J. Exp. Med. (1990) 171:265-297
  #title   Anti-DNA antibodies from autoimmune mice arise by clonal
            expansion and somatic mutation.
  #cross-references MUID:90111618
  #accession PL0262
            ##molecule_type mRNA
            ##residues 1-106 ##label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin
KEYWORDS   heterotetramer; immunoglobulin homology
FEATURE
   1-23   #region framework 1\
   24-34.   #region complementarity-determining 1\
   35-49   #region framework 2\
   50-56   #region complementarity-determining 2\
   57-88   #region framework 3\
   89-97   #region complementarity-determining 3\
   98-106   #region framework 4
SUMMARY   #length 106 #checksum 658

Db   79 ESEDFADY 87
           ||||| ||
Qy   99 ESEDFVAYY 107

Query Match   83.8%; Score 57; DB 2; Length 106;
Best Local Similarity   77.8%; Pred. No. 6.94e+00;
Matches   7; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

RESULT   12
ENTRY   B47271   #type fragment
TITLE   nitrophenyl phosphonate-specific antibody 48G7 light chain VJ
            - synthetic (fragment)
ORGANISM   #formal_name synthetic
   #note   Mus musculus (house mouse) gene engineered and expressed in
            Escherichia coli
DATE   21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change
            11-Aug-1995
ACCESSIONS B47271
REFERENCE   B47271
  #authors Lesley, S.A.; Patten, P.A.; Schultz, P.G.
  #journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1160-1165
  #title   A genetic approach to the generation of antibodies with
            enhanced catalytic activities.
  #cross-references MUID:93165560
  #accession B47271
            ##molecule_type DNA; protein
            ##residues 1-108 ##label LES
   ##note   sequence extracted from NCBI backbone (NCBIN:124856,
            NCBIP:124859)
   ##note   parts of this sequence were determined by protein
            sequencing
FEATURE
   24-89   #disulfide_bonds #status predicted
SUMMARY   #length 108 #checksum 9036

Db   80 ESEDFADY 88
           ||||| ||
Qy   99 ESEDFVAYY 107

Query Match   83.8%; Score 57; DB 4; Length 108;
Best Local Similarity   77.8%; Pred. No. 6.94e+00;
Matches   7; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

RESULT   13
ENTRY   KVMS3B   #type complete
TITLE   Ig kappa chain precursor V region (VKM173B) - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change
            20-Mar-1998
ACCESSIONS A01924
REFERENCE   A01924
  #authors Max, E.E.; Seidman, J.G.; Miller, H.; Leder, P.
  #journal Cell (1980) 21:793-799
  #title   Variation in the crossover point of kappa immunoglobulin gene
            V-J recombination: evidence from a cryptic gene.
  #cross-references MUID:81064681
  #accession A01924
            ##molecule_type DNA
            ##residues 1-117 ##label MAX
GENETICS
   #introns 19/1
COMPLEX   An immunoglobulin heterotetramer subunit consists of two
            identical light (kappa or lambda) and two identical heavy
            (alpha, delta, epsilon, gamma, or mu) chains usually
            stabilized by interchain disulfide bonds. In some cases,
            such as IgA and IgM, the subunits associate into larger
            oligomers.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer
FEATURE
   1-22   #domain signal sequence #status predicted #label SIG\
   23-117   #product Ig kappa chain V region (VKM173B) #status
              predicted #label MAT\
   45-110   #disulfide_bonds #status predicted
SUMMARY   #length 117 #molecular-weight 12954 #checksum 3822

Query Match   83.8%; Score 57; DB 1; Length 117;
Best Local Similarity   77.8%; Pred. No. 6.94e+00;

```
Matches    7;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Db   101 ESEDFADYY 109
         ||||| ||
Qy    99 ESEDFVAYY 107


RESULT   14

ENTRY       D32513         #type complete
TITLE       Ig kappa chain precursor V region (BXW16) - mouse
ORGANISM    #formal_name Mus musculus #common_name house mouse
DATE        21-May-1990 #sequence_revision 31-Dec-1990 #text_change
            20-Mar-1998
ACCESSIONS  D32513
REFERENCE   A94689
  #authors  Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.;
            Noonan, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos,
            A.N.
  #journal  J. Clin. Invest. (1988) 82:852-860
  #title    Immunoglobulin kappa light chain variable region gene complex
            organization and immunoglobulin genes encoding anti-DNA
            autoantibodies in lupus mice.
  #cross-references MUID:88331394
  #accession D32513
    ##molecule_type DNA
    ##residues 1-129 ##label KOF
    ##cross-references GB:M20832; NID:g196941; PID:g196942
CLASSIFICATION  #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS    heterotetramer; immunoglobulin
SUMMARY     #length 129 #molecular-weight 14097 #checksum 3457

Query Match      83.8%;    Score 57;  DB 2;  Length 129;
Best Local Similarity  77.8%;    Pred. No. 6.94e+00;
Matches   7;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Db   101 ESEDFADYY 109
         ||||| ||
Qy    99 ESEDFVAYY 107


RESULT   15

ENTRY       S34090         #type complete
TITLE       Ig kappa chain V region - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
            09-May-1997
ACCESSIONS  S34090
REFERENCE   S34076
  #authors  Wagner, S.D.; Luzzatto, L.
  #journal  Eur. J. Immunol. (1993) 23:391-397
  #title    V-kappa gene segments rearranged in chronic lymphocytic
            leukemia are distributed over a large portion of the
            V-kappa locus and do not show somatic mutation.
  #accession S34090
    ##status preliminary
    ##molecule_type DNA
    ##residues 1-82 ##label WAG
    ##cross-references EMBL:X67174
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS    heterotetramer; immunoglobulin
SUMMARY     #length 82 #molecular-weight 8891 #checksum 4385

Query Match      82.4%;    Score 56;  DB 2;  Length 82;
Best Local Similarity  66.7%;    Pred. No. 1.01e+01;
Matches   6;  Conservative   2;  Mismatches   1;  Indels   0;  Gaps   0;

Db    70 OSEDFAIYY 78
         :||| ||  :||
Qy    99 ESEDFVAYY 107
```

Search completed: Tue Apr 20 14:01:25 1999
Job time : 18 secs.

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MPSRCH (TM)

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

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Run on: Tue Apr 20 13:59:47 1999; MasPar time 2.35 Seconds
                 102.676 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence:

>US-08-836-455-2
(99-107) from US08836455.pep (3 of 3)
68
1 ESEDVAYY 9

Scoring table: PAM 150
                 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: swiss-prot35
                 1:swissprot

Statistics: Mean 25.463; Variance 33.115; scale 0.769

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	64	94.1	130	1	KV5G_MOUSE	IG KAPPA CHAIN PRECURS	3.87e-02
2	57	83.8	117	1	KV5H_MOUSE	IG KAPPA CHAIN PRECURS	1.05e+00
3	56	82.4	108	1	KV5K_HUMAN	IG KAPPA CHAIN V-I REG	1.65e+00
4	56	82.4	108	1	KV1N_HUMAN	IG KAPPA CHAIN V-I REG	1.65e+00
5	56	82.4	613	1	UL06_EBV	VIRION PROTEIN BBRF1.	1.65e+00
6	55	80.9	107	1	KV1D_HUMAN	IG KAPPA CHAIN V-I REG	2.58e+00
7	54	79.4	100	1	KV3C_HUMAN	IG KAPPA CHAIN PRECURS	4.01e+00
8	54	79.4	108	1	KV3A_HUMAN	IG KAPPA CHAIN V-III R	4.01e+00
9	54	79.4	109	1	KV3F_HUMAN	IG KAPPA CHAIN V-III R	4.01e+00
10	54	79.4	109	1	KV3D_HUMAN	IG KAPPA CHAIN V-III R	4.01e+00
11	54	79.4	109	1	KV3E_HUMAN	IG KAPPA CHAIN V-III R	4.01e+00
12	54	79.4	109	1	KV3G_HUMAN	IG KAPPA CHAIN V-III R	4.01e+00
13	54	79.4	112	1	KV1U_HUMAN	IG KAPPA CHAIN V-I REG	4.01e+00
14	54	79.4	115	1	KV3I_HUMAN	IG KAPPA CHAIN PRECURS	4.01e+00
15	54	79.4	128	1	KV3R_HUMAN	IG KAPPA CHAIN PRECURS	4.01e+00
16	54	79.4	129	1	KV3H_HUMAN	IG KAPPA CHAIN PRECURS	4.01e+00
17	54	79.4	129	1	KV3L_HUMAN	IG KAPPA CHAIN PRECURS	4.01e+00
18	53	77.9	108	1	KV1C_HUMAN	IG KAPPA CHAIN V-I REG	6.19e+00
19	53	77.9	108	1	KV1G_HUMAN	IG KAPPA CHAIN V-I REG	6.19e+00
20	53	77.9	108	1	KV1H_HUMAN	IG KAPPA CHAIN V-I REG	6.19e+00
21	53	77.9	108	1	KV1V_HUMAN	IG KAPPA CHAIN V-I REG	6.19e+00
22	53	77.9	108	1	KV1R_HUMAN	IG KAPPA CHAIN V-III R	6.19e+00
23	53	77.9	109	1	KV3B_HUMAN	IG KAPPA CHAIN V-III R	6.19e+00
24	53	77.9	53	1	KV1I_HUMAN	IG KAPPA CHAIN PRECURS	6.19e+00
25	53	77.9	129	1	KV1X_HUMAN	IG KAPPA CHAIN PRECURS	6.19e+00
26	53	77.9	53	1	YFPA_ECOLI	HYPOTHETICAL 64.5 KD P	6.19e+00
27	53	77.9	578	1	VEF_GVTIN	VIRAL ENHANCING FACTOR	6.19e+00
28	53	77.9	901	1	VEF_GVPU	VIRAL ENHANCING FACTOR	6.19e+00
29	52	76.5	901	1	KV1L_HUMAN	IG KAPPA CHAIN V-I REG	9.51e+00
30	52	76.5	108	1	KV1F_HUMAN	IG KAPPA CHAIN V-I REG	9.51e+00
31	52	76.5	108	1	KV1T_HUMAN	IG KAPPA CHAIN V-I REG	9.51e+00
32	52	76.5	109	1	KV1J_HUMAN	IG KAPPA CHAIN V-I REG	9.51e+00
33	52	76.5	117	1	END_HELPY	ENOLASE (EC 4.2.1.11)	9.51e+00
34	52	76.5	259	1	IF2C_CYACA	TRANSLATION INITIATION	9.51e+00
35	51	75.0	715	1	ADSV_MOUSE	ADSEVERIN (SCINDERIN)	9.51e+00
36	51	75.0	715	1	ADSV_BOVIN	ADSEVERIN (SCINDERIN)	1.45e+01
37	51	75.0	408	1	KV3J_HUMAN	IG KAPPA CHAIN PRECURS	1.45e+01
38	51	75.0	116	1	YJ95_YEAST	HYPOTHETICAL 45.1 KD P	1.45e+01
39	50	73.5	108	1	KV5D_MOUSE	IG KAPPA CHAIN V-V REG	2.20e+01
40	50	73.5	115	1	KV1E_HUMAN	IG KAPPA CHAIN V-I REG	2.20e+01
41	50	73.5	426	1	KV5C_MOUSE	IG KAPPA CHAIN PRECURS	2.20e+01
42	50	73.5	510	1	BAGT_MOUSE	BETA-1,4 N-ACETYLGALAC	2.20e+01
43	50	73.5	883	1	CAPP_ECOLI	PHOSPHOENOLPYRUVATE CA	2.20e+01
44	50	73.5	936	1	CAPP_RHOPA	PHOSPHOENOLPYRUVATE CA	2.20e+01
45	50	73.5	1004	1	YD83_SCHPO	HYPOTHETICAL 112.0 KD	2.20e+01

ALIGNMENTS

RESULT   1
ID   KV5G_MOUSE   STANDARD;   PRT;   130 AA.
AC   P01639; P01640;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 41).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 79221900.
RA   SEIDMAN J.G., MAX E.E., LEDER P.;
RL   NATURE 280:370-375(1979).
RN   [2]
RP   SEQUENCE OF 1-33.
RX   MEDLINE; 77148916.
RA   BURSTEIN Y., SCHECHTER I.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 74:716-720(1977).
RN   [3]
RP   SEQUENCE OF 23-130.
RX   MEDLINE; 67056897.
RA   GRAY W.R., DREYER W.J., HOOD L.;
RL   SCIENCE 155:465-467(1967).
CC   -!- THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE SYSTEM DIRECTED BY
CC   MRNA ISOLATED FROM MYELOMA POLYSOMES.
CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01922; KVMSM4.
HSSP; P01607; 6FAB.
KW   IMMUNOGLOBULIN V REGION; SIGNAL; BENCE-JONES PROTEIN.
FT   SIGNAL   1   22
FT   CHAIN   23   130   IG KAPPA CHAIN V-V REGION (MOPC 41).
FT   DOMAIN   23   45   FRAMEWORK 1.
FT   DOMAIN   46   56   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   57   71   FRAMEWORK 2.
FT   DOMAIN   72   78   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   79   110   FRAMEWORK 3.
FT   DOMAIN   111   119   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   120   129   FRAMEWORK 4.
FT   VARIANT   1   2   MISSING (IN 25% OF THE MOLECULES).
FT   DISULFID   45   110   BY SIMILARITY.
FT   NON_TER   130   130
SQ   SEQUENCE   130 AA;   14311 MW;   E77D75A2 CRC32;

Query Match   94.1%;   Score 64;   DB 1;   Length 130;
Best Local Similarity 88.9%;   Pred. No. 3.87e-02;

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Db  101 ESEDFVDIY 109
            |||||| ||
Qy   99 ESEDFVAYY 107

Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;


RESULT 2

ID   KV5H_MOUSE      STANDARD;      PRT;      117 AA.
AC   P01641;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 173B).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RL   SEQUENCE FROM N.A.
RX   MEDLINE; 81064681.
RA   MAX E.E., SEIDMAN J.G., MILLER H., LEDER P.;
RL   CELL 21:793-799(1980).
DR   EMBL; K00880; G197444; -.
DR   PIR; A01924; KVMS3B.
DR   HSSP; P01607; 1FGV.
KW   IMMUNOGLOBULIN V REGION; SIGNAL.
FT   SIGNAL         1     22
FT   CHAIN         23    117       IG KAPPA CHAIN V-V REGION (MOPC 173B).
FT   DOMAIN        23     45       FRAMEWORK 1.
FT   DOMAIN        46     56       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        57     71       FRAMEWORK 2.
FT   DOMAIN        72     78       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        79    110       FRAMEWORK 3.
FT   DOMAIN       111   >117       COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID      45    110       BY SIMILARITY.
FT   NON_TER      117    117
SQ   SEQUENCE     117 AA;   12954 MW;   38F2B08C CRC32;


Query Match     83.8%;   Score 57;   DB 1;   Length 117;
Best Local Similarity  77.8%;   Pred. No. 1.05e+00;
Matches     7;   Conservative     0;   Mismatches     2;   Indels     0;   Gaps     0;

Db  101 ESEDFADY 109
            ||||| ||
Qy   99 ESEDFVAYY 107


RESULT 3

ID   KV1K_HUMAN      STANDARD;      PRT;      108 AA.
AC   P01603;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (KA).
RN   [1]
RA   SHINODA T.;
RL   J. BIOCHEM. 77:1277-1296(1975).
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01869; KIHUKA.
DR   HSSP; P01607; 1IGM.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT   DOMAIN         1     23       FRAMEWORK 1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    107       FRAMEWORK 4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE     108 AA;   11900 MW;   41BC730E CRC32;


Query Match     82.4%;   Score 56;   DB 1;   Length 108;
Best Local Similarity  33.3%;   Pred. No. 1.65e+00;
Matches     3;   Conservative     5;   Mismatches     1;   Indels     0;   Gaps     0;

Db   79 ZPZBFATY 87
            :::|| :||
Qy   99 ESEDFVAYY 107


RESULT 4

ID   KV1N_HUMAN      STANDARD;      PRT;      108 AA.
AC   P01606;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (OU).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RL   SEQUENCE.
RX   MEDLINE; 70201507.
RA   KOHLER H., SHIMIZU A., PAUL C., PUTNAM F.W.;
RL   SCIENCE 169:56-59(1970).
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
DR   PIR; A01872; KIHUOU.
DR   HSSP; P01607; 2FGW.
KW   IMMUNOGLOBULIN V REGION.
FT   DOMAIN         1     23       FRAMEWORK 1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    107       FRAMEWORK 4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE     108 AA;   11777 MW;   4B089785 CRC32;


Query Match     82.4%;   Score 56;   DB 1;   Length 108;
Best Local Similarity  33.3%;   Pred. No. 1.65e+00;
Matches     3;   Conservative     5;   Mismatches     1;   Indels     0;   Gaps     0;

Db   79 ZPZBFAIY 87
            :::|| :||
Qy   99 ESEDFVAYY 107


RESULT 5

ID   UL06_EBV      STANDARD;      PRT;      613 AA.
AC   P03213;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE   VIRION PROTEIN BBRF1.
GN   BBRF1.
OS   EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
OC   VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; GAMMAHERPESVIRINAE.
RN   [1]
RL   SEQUENCE FROM N.A.
RX   MEDLINE; 84270667.
RA   BAER R., BANKIER A.T., BIGGIN M.D., DEININGER P.L., FARRELL P.J.,
RA   GIBSON T.J., HATFULL G., HUDSON G.S., SATCHWELL S.C., SEGUIN C.,
RA   TUFFNELL P.S., BARRELL B.G.;
RL   NATURE 310:207-211(1984).
CC   -!- FUNCTION: PRESUMED VIRION PROTEIN; POSSIBLE ROLE IN DNA
CC       PACKAGING (BY SIMILARITY).
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CC   -!- SIMILARITY: BELONGS TO FAMILY THAT-GROUPS TOGETHER HSV-1 UL6,
CC        EHV-1 56, EBV BBRF1, HCMV UL104, AND VZV 54.
DR   EMBL; V01555; G59125; -.
DR   PIR; A03775; QOBE33.
DR   PIR; S33025; S33025.
KW   LATE PROTEIN.
SQ   SEQUENCE   613 AA;  68456 MW;  69A44AE8 CRC32;

Matches       5; Conservative   3; Mismatches   0; Indels    0; Gaps    0;
Best Local Similarity  62.5%; Pred. No. 1.65e+00;
Query Match    82.4%; Score 56; DB 1; Length 613;

Qy    100 SDEDFVAYY  107
          |:||| ||||
Db    221 SDEYVAYY  228

RESULT  6
ID   KVID_HUMAN  STANDARD;  PRT;  107 AA.
AC   P01596;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (CAR).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 75075135.
RA   MILSTEIN C.P., DEVERSON E.V.;
RL   EUR. J. BIOCHEM. 49:377-391(1974).
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC   -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01864; KIHUAR.
     HSSP; P01607; 1DFB.
KW   IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT   CARBOHYD     28     28
FT   NON_TER     107    107
SQ   SEQUENCE  107 AA;  11703 MW;  04BF9EFD CRC32;

Matches       3; Conservative   5; Mismatches   1; Indels    0; Gaps    0;
Best Local Similarity  33.3%; Pred. No. 2.58e+00;
Query Match    80.9%; Score 55; DB 1; Length 107;

Qy     99 ESEDFVAYY  107
          ::||| |||
Db     79 ZPBBFATYY  87

RESULT  7
ID   KV3C_HUMAN  STANDARD;  PRT;  100 AA.
AC   P01621;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-III REGION (NG9) (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 84093600.
RA   BENTLEY D.L.;
RL   NATURE 307:77-80(1984);
CC   -!- THIS GENE WAS ISOLATED FROM THE NG9/9.1 HYBRIDOMA.
DR   PIR; A01894; K3HUNG.
     HSSP; P01607; 1AAG.
KW   IMMUNOGLOBULIN V REGION; SIGNAL; HYBRIDOMA.
FT   NON_TER       1      1
FT   SIGNAL       <1      4
FT   CHAIN         5    100
FT   DISULFID     27     93
FT                            IG KAPPA CHAIN V-III REGION (NG9).
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FT   NON_TER     100    100
SQ   SEQUENCE  100 AA;  10729 MW;  99A75223 CRC32;

Matches       6; Conservative   1; Mismatches   2; Indels    0; Gaps    0;
Best Local Similarity  66.7%; Pred. No. 4.01e+00;
Query Match    79.4%; Score 54; DB 1; Length 100;

Qy     99 ESEDFVAYY  107
          ||||| ||
Db     84 EPEDFAVYY  92

RESULT  8
ID   KV3A_HUMAN  STANDARD;  PRT;  108 AA.
AC   P01619;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-III REGION (B6).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RA   MILSTEIN C.;
RL   FEBS LETT. 2:301-304(1969).
CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01891; K3HUB5.
     HSSP; P01607; 1MCP.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT   DISULFID     23     89  BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE  108 AA;  11635 MW;  46D6868E CRC32;

Matches       5; Conservative   2; Mismatches   2; Indels    0; Gaps    0;
Best Local Similarity  55.6%; Pred. No. 4.01e+00;
Query Match    79.4%; Score 54; DB 1; Length 108;

Qy     99 ESEDFVAYY  107
          ::||| ||
Db     80 ZPEDFAVYY  88

RESULT  9
ID   KV3F_HUMAN  STANDARD;  PRT;  109 AA.
AC   P01624;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-III REGION (POM).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RA   KLAPPER D.G., CAPRA J.D.;
RL   ANN. INST. PASTEUR IMMUNOL. 127C:261-271(1976).
CC   -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC       ACTIVITY.
DR   PIR; A01897; K3HUPM.
     HSSP; P01607; 1DFB.
KW   IMMUNOGLOBULIN V REGION.
FT   DISULFID     23     89  BY SIMILARITY.
FT   NON_TER     109    109
SQ   SEQUENCE  109 AA;  11922 MW;  A0C42C88 CRC32;

Matches       6; Conservative   1; Mismatches   2; Indels    0; Gaps    0;
Best Local Similarity  66.7%; Pred. No. 4.01e+00;
Query Match    79.4%; Score 54; DB 1; Length 109;

Qy     99 ESEDFVAYY  107
          :||| ||
Db     80 QSEDFAVYY  88
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RESULT 10

ID   KV3D_HUMAN   STANDARD;   PRT;   109 AA.
AC   P01622;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-III REGION (TI).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 72188439.
RA   SUTER L., BARNIKOL H.U., WATANABE S., HILSCHMANN N.;
RL   HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 353:189-208(1972).
CC   -!- THIS IS A BENCE-JONES PROTEIN.
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR   PIR; A01895; K3HUTI.
DR   HSSP; P01607; 2IMM.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT   DISULFID   23   89   BY SIMILARITY.
FT   NON_TER   109   109
SQ   SEQUENCE   109 AA; 11788 MW; D03795B1 CRC32;

Query Match   79.4%; Score 54; DB 1; Length 109;
Best Local Similarity   66.7%; Pred. No. 4.01e+00;
Matches   6; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Db   80 EPEDFAVYY 88
               |:||| ||
Qy   99 ESEDFVAYY 107

RESULT 11

ID   KV3E_HUMAN   STANDARD;   PRT;   109 AA.
AC   P01623;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-III REGION (WOL).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 82046598.
RA   ANDREWS D.W., CAPRA J.D.;
RL   BIOCHEMISTRY 20:5816-5822(1981).
CC   -!- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC   ACTIVITY.
DR   PIR; A01896; K3HUWL.
DR   HSSP; P01607; 1DFB.
KW   IMMUNOGLOBULIN V REGION.
FT   DISULFID   23   89
FT   NON_TER   109   109   BY SIMILARITY.
SQ   SEQUENCE   109 AA; 11746 MW; 7D8F5D75 CRC32;

Query Match   79.4%; Score 54; DB 1; Length 109;
Best Local Similarity   66.7%; Pred. No. 4.01e+00;
Matches   6; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Db   80 EPEDFAVYY 88
               |:||| ||
Qy   99 ESEDFVAYY 107

RESULT 12

ID   KV3G_HUMAN   STANDARD;   PRT;   109 AA.
AC   P04206;
DT   20-MAR-1987 (REL. 04, CREATED)
DT   20-MAR-1987 (REL. 04, LAST SEQUENCE UPDATE)

RESULT 13

ID   KV1U_HUMAN   STANDARD;   PRT;   112 AA.
AC   P01613;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (NI).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RX   MEDLINE; 73191505.
RA   SHINODA T.;
RL   J. BIOCHEM. 73:433-446(1973).
CC   -!- THIS IS A BENCE-JONES PROTEIN.
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR   PIR; A01880; K1HUNV.
DR   HSSP; P01607; 1FVD.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT   DISULFID   23   92   BY SIMILARITY.
FT   NON_TER   112   112
SQ   SEQUENCE   112 AA; 12246 MW; A30F576F CRC32;

Query Match   79.4%; Score 54; DB 1; Length 112;
Best Local Similarity   33.3%; Pred. No. 4.01e+00;
Matches   6; Conservative   4; Mismatches   2; Indels   0; Gaps   0;

Db   83 ZPZBFAVYY 91
               :::| ||
Qy   99 ESEDFVAYY 107

RESULT 14

ID   KV3I_HUMAN   STANDARD;   PRT;   115 AA.
AC   P04433;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT   01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85087932.
RA   PECH M., ZACHAU H.G.;

DT   20-MAR-1987 (REL. 04, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-III REGION (GOL) (RHEUMATOID FACTOR).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 86230578.
RA   NEWKIRK M., CHEN P.P., CARSON D.A., POSNETT D., CAPRA J.D.;
RL   MOL. IMMUNOL. 23:239-244(1986).
DR   PIR; A01893; K3HUGO.
DR   HSSP; P01607; 1DFB.
KW   IMMUNOGLOBULIN V REGION.
FT   DISULFID   23   89
FT   NON_TER   109   109   BY SIMILARITY.
SQ   SEQUENCE   109 AA; 11830 MW; 893DCC4A CRC32;

Query Match   79.4%; Score 54; DB 1; Length 109;
Best Local Similarity   66.7%; Pred. No. 4.01e+00;
Matches   6; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Db   80 EPEDFAVYY 88
               |:||| ||
Qy   99 ESEDFVAYY 107

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RL   NUCLEIC ACIDS RES. 12:9229-9236(1984).
DR   EMBL; X01668; -; NOT_ANNOTATED_CDS.
DR   PIR; A01900; K3HUVG.
DR   HSSP; P01607; 1AAG.
KW   IMMUNOGLOBULIN V REGION; SIGNAL.
FT   SIGNAL         1     20
FT   CHAIN         21   >115       IG KAPPA CHAIN V-III REGION (VG).
FT   DOMAIN        21     43       FRAMEWORK 1.
FT   DOMAIN        44     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        55     69       FRAMEWORK 2.
FT   DOMAIN        70     76       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        77    108       FRAMEWORK 3.
FT   DOMAIN       109    115       COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID      43    108       BY SIMILARITY.
FT   NON_TER      115    115
SQ   SEQUENCE     115 AA;    12575 MW;   37E182FC CRC32;

Db       99  EPEDFAVYY 107
             |:|||  ||
Qy       99  ESEDFVAYY 107

     Query Match              79.4%;    Score 54;    DB 1;   Length 115;
     Best Local Similarity   66.7%;     Pred. No. 4.01e+00;
     Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;


RESULT   15
ID   KV3K_HUMAN     STANDARD;     PRT;     128 AA.
AC   P06311;
DT   01-JAN-1988  (REL. 06, CREATED)
DT   01-JAN-1988  (REL. 06, LAST SEQUENCE UPDATE)
DT   01-NOV-1990  (REL. 16, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-III REGION (IARC/BL41).
OS   HOMO SAPIENS (HUMAN)
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 86041852.
RA   KLOBECK H.G., MEINDL A., COMBRIATO G., SOLOMON A., ZACHAU H.G.;
RL   NUCLEIC ACIDS RES. 13:6499-6513(1985).
DR   EMBL; Z00021; G33179; -.
DR   PIR; A01899; K3HU41.
DR   HSSP; P01607; 3HFM.
KW   IMMUNOGLOBULIN V REGION; SIGNAL.
FT   SIGNAL         1     20
FT   CHAIN         21    128       IG KAPPA CHAIN V-III REGION (IARC/BL41).
FT   DOMAIN        21     43       FRAMEWORK 1.
FT   DOMAIN        44     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        55     69       FRAMEWORK 2.
FT   DOMAIN        70     76       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        77    108       FRAMEWORK 3.
FT   DOMAIN       109    117       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       118    128       JK1 SEGMENT.
FT   DISULFID      43    108       BY SIMILARITY.
FT   NON_TER      128    128
SQ   SEQUENCE     128 AA;    14070 MW;   318E08AF CRC32;

Db       99  EPEDFAVYY 107
             |:|||  ||
Qy       99  ESEDFVAYY 107

     Query Match              79.4%;    Score 54;    DB 1;   Length 128;
     Best Local Similarity   66.7%;     Pred. No. 4.01e+00;
     Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;
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Search completed: Tue Apr 20 13:59:53 1999
Job time : 6 secs.

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*******************************************************************
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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

n on: Tue Apr 20 14:00:10 1999; MasPar time 4.37 Seconds
                                       102.577 Million cell updates/sec

Tabular output not generated.

Title: >US-08-836-455-2
Description: (99-107) from US08836455.pep (3 of 3)
Perfect Score: 68
Sequence: 1 ESEDFVAYY 9

Scoring table: PAM 150
                Gap 11

Searched: 165420 seqs, 4979564 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: sptrembl6
                1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
                5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
                9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
                13:sp_vertebrate 14:sp_virus

Statistics: Mean 24.693; Variance 34.950; scale 0.707

                Pred. No. is the number of results predicted by chance to have a
                score greater than or equal to the score of the result being printed,
                and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	56	82.4	236	1	P99945	ENDONUCLEASE III.	4.58e+00
2	56	82.4	771	11	Q63693	PHODPHOLIPASE C DELTA4	4.58e+00
3	56	82.4	772	11	Q62711	PHOSPHOLIPASE C DELTA-	4.58e+00
4	54	79.4	108	4	Q99818	ANTI-SSDNA ANTIBODY LI	1.06e+01
5	54	79.4	113	4	Q14539	HRV FAB 026-VL (FRAGME	1.06e+01
6	54	79.4	114	4	Q14538	HRV FAB 026-VL (FRAGME	1.06e+01
7	54	79.4	115	4	Q14537	HRV FAB N28-VL (FRAGME	1.06e+01
8	54	79.4	251	3	042983	HYPOTHETICAL 28.9 KD P	1.06e+01
9	54	79.4	504	4	Q13217	PROTEIN KINASE INHIBIT	1.06e+01
10	54	79.4	504	6	060873	PROTEIN KINASE, INTERF	1.06e+01
11	54	79.4	504	6	027968	PKR INHIBITOR P58.	1.06e+01
12	53	77.9	81	11	061588	G8(ANTI-MRBC HYBRIDOMA	1.06e+01
13	53	77.9	93	4	Q16078	RF-V KAPPA 1-RHEUMATOI	1.06e+01
14	53	77.9	94	4	Q16079	RF-V KAPPA 1-RHEUMATOI	1.06e+01
15	53	77.9	105	4	Q99514	LIGHT CHAIN FAB FRAGME	1.06e+01
16	53	77.9	112	4	Q99822	ANTI-HIV-1 GP120 ANTIB	1.06e+01
17	53	77.9	113	4	014540	HRV FAB 027-VL (FRAGME	1.06e+01
18	53	77.9	113	4	014355	HRV FAB N6-VL (FRAGMEN	1.06e+01
19	53	77.9	117	4	013358	IMMUNOGLOBULIN VARIABL	1.60e+01
20	53	77.9	217	5	Q27727	Y-BOX BINDING PROTEIN	1.60e+01
21	53	77.9	290	2	051169	GLYCINE BETAINE, L-PRO	1.60e+01
22	53	77.9	474	5	044413	T07A9.2 PROTEIN.	1.60e+01
23	53	77.9	562	2	P76523	SIMILAR TO.	1.60e+01
24	52	76.5	116	4	Q15982	RHEUMATOID FACTOR C6 L	2.40e+01
25	52	76.5	239	4	043690	ANTI-MPL SCFV (FRAGMEN	2.40e+01
26	52	76.5	240	4	000289	SINGLE-CHAIN FV FRAGME	2.40e+01
27	52	76.5	244	4	043689	ANTI-HER3 SCFV (FRAGME	2.40e+01
28	52	76.5	244	4	000288	SINGLE-CHAIN FV FRAGME	2.40e+01
29	52	76.5	373	5	061088	HYPOTHETICAL 42.0 KD P	2.40e+01
30	52	76.5	494	3	013601	HYPOTHETICAL 68.1 KD P	2.40e+01
31	52	76.5	590	2	008990	PI006 PROTEIN.	2.40e+01
32	52	76.5	615	11	051516	HYPOTHETICAL 68.1 KD P	2.40e+01
33	52	76.5	835	2	P74210	ADSEVERIN.	2.40e+01
34	52	76.5	1434	5	062229	NITROGEN ASSIMILATION	2.40e+01
35	51	75.0	265	1	026562	F44G3.8.	3.58e+01
36	51	75.0	294	5	019891	HYPOTHETICAL 31.5 KD P	3.58e+01
37	51	75.0	435	10	023097	F28H7.3	3.58e+01
38	51	75.0	833	3	005787	BAC TM018A10.	3.58e+01
39	51	75.0	102	11	P97408	CHROMOSOME XII COSMID	3.58e+01
40	50	73.5	337	2	051275	TYPE II COLLAGEN ANTIB	5.32e+01
41	50	73.5	540	5	017756	HYPOTHETICAL 39.1 KD P	5.32e+01
42	50	73.5	596	5	045633	F01D4.1.	5.32e+01
43	50	73.5	687	14	088271	K01G12.3.	5.32e+01
44	50	73.5	3212	5	Q94010	NON-STRUCTURAL PROTEIN	5.32e+01
45	49	72.1	543	14	055339	SPIKE GLYCOPROTEIN S1	7.85e+01

ALIGNMENTS

RESULT 1
ID   P95945;   PRELIMINARY;   PRT;   236 AA.
AC   P95945;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   ENDONUCLEASE III.
OS   SULFOLOBUS SOLFATARICUS.
OC   ARCHAEBACTERIA; CRENARCHAEOTA; SULFOLOBALES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2;
RX   MEDLINE; 97055432.
RA   SENSEN C.W., KLENK H.P., SINGH R.K., ALLARD G., CHAN C.C.Y., LIU Q.Y.,
RA   PENNY S.L., YOUNG F., SCHENK M.E., GAASTERLAND T., DOOLITTLE W.F.,
RA   RAGAN M.A., CHARLEBOIS R.L.;
RL   MOL. MICROBIOL. 22:175-191(1996).
DR   EMBL; Y08257; E283822; -.
DR   PFAM; PF00730; Endonuclease_3.
KW   ENDONUCLEASE.
SQ   SEQUENCE   236 AA;   26843 MW;   31E2C546 CRC32;

Query Match   82.4%; Score 56; DB 1; Length 236;
Best Local Similarity 85.7%;
Matches   6; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   21 EDFIAYY 27
            |||:|||
Db   101 EDFVAYY 107

RESULT 2
ID   Q63693;   PRELIMINARY;   PRT;   771 AA.
AC   Q63693;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   PHODPHOLIPASE C DELTA4.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DONRYU;
```

RX   MEDLINE; 96132927.
RA   LIU N., FUKAMI K., YU H., TAKENAWA T.;
RL   J. BIOL. CHEM. 271:355-360(1996).
DR   EMBL; D50455; G1304189; -.
DR   PFAM; PF00036; efhand.
DR   PFAM; PF00168; C2.
DR   PFAM; PF00387; PI-PLC-Y.
DR   PFAM; PF00388; PI-PLC-X.
SQ   SEQUENCE   771 AA; 88862 MW; F347F051 CRC32;

Qy   99 ESEDFVAYY 107

Db   191 DSEEFVQFY 199
Query Match   82.4%; Score 56; DB 11; Length 771;
Best Local Similarity   55.6%; Pred. No. 4.58e+00;
Matches   5; Conservative   3; Mismatches   1; Indels   0; Gaps   0;

RESULT 3
ID   Q62711;   PRELIMINARY;   PRT;   772 AA.
AC   Q62711;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   PHOSPHOLIPASE C DELTA-4.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE DAWLEY; TISSUE=BRAIN;
RX   MEDLINE; 96132878.
RA   LEE S.B., RHEE S.G.;
RL   J. BIOL. CHEM. 271:25-31(1996).
DR   EMBL; U16655; G571466; -.
DR   PFAM; PF00036; efhand.
DR   PFAM; PF00168; C2.
DR   PFAM; PF00387; PI-PLC-Y.
DR   PFAM; PF00388; PI-PLC-X.
SQ   SEQUENCE   772 AA; 88966 MW; 6FE7ACA1 CRC32;

Qy   99 ESEDFVAYY 107

Db   191 DSEEFVQFY 199

RESULT 4
ID   Q99818;   PRELIMINARY;   PRT;   108 AA.
AC   Q99818;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   ANTI-SSDNA ANTIBODY LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN   HUMKV328H5.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SUENAGA R.;
RL   SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U82258; G1773057; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER   1   1
SQ   SEQUENCE   108 AA; 11792 MW; 876D5BA3 CRC32;

Query Match   79.4%; Score 54; DB 4; Length 108;

Best Local Similarity   66.7%; Pred. No. 1.06e+01;
Matches   6; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Qy   99 ESEDFVAYY 107

Db   79 QSEDFVAYY 87

RESULT 5
ID   O14539;   PRELIMINARY;   PRT;   113 AA.
AC   O14539;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   HRV FAB 026-VL (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PBL;
RA   ITOH K., SUZUKI T.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB006848; D1023046; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER   113   113
SQ   SEQUENCE   113 AA; 11994 MW; 3CA4456F CRC32;

Qy   99 ESEDFVAYY 107

Db   81 EPEDFVAYY 89
Query Match   79.4%; Score 54; DB 4; Length 113;
Best Local Similarity   66.7%; Pred. No. 1.06e+01;
Matches   6; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

RESULT 6
ID   O14538;   PRELIMINARY;   PRT;   114 AA.
AC   O14538;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   HRV FAB N28-VL (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PBL;
RA   ITOH K., SUZUKI T.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB006845; D1023044; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER   114   114
SQ   SEQUENCE   114 AA; 12283 MW; BFE57FD0 CRC32;

Qy   99 ESEDFVAYY 107

Db   82 EPEDFVAYY 90
Query Match   79.4%; Score 54; DB 4; Length 114;
Best Local Similarity   66.7%; Pred. No. 1.06e+01;
Matches   6; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

RESULT 7
ID   O14537;   PRELIMINARY;   PRT;   115 AA.
AC   O14537;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   HRV FAB N27-VL (FRAGMENT).

OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PBL;
RA   ITOH K., SUZUKI T.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB006844; D1023043; -.
DR   PFAM; PF00047; ig.
FT   NON_TER   115   115
SQ   SEQUENCE   115 AA;   12417 MW; 96E3C279 CRC32;

Query Match   79.4%; Score 54; DB 4; Length 115;
Best Local Similarity   66.7%; Pred. No. 1.06e+01;
Matches   6; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Db   82 EPEDFAVYY 90
              |:||| ||
Qy   99 ESEDFVAYY 107

RESULT 8
ID   Q42983   PRELIMINARY;   PRT;   251 AA.
AC   Q42983;
DT   01-JUN-1998 (TREMBLREL. 06, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 28.9 KD PROTEIN.
GN   SPBC24E9.03C
OS   SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972H-;
RA   LYNE M., PURNELLE B., GOFFEAU A., WOOD V., RAJANDREAM M.A.,
RA   BARRELL B.G.;
RL   SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AL021816; E1250650; -.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   251 AA;   28915 MW; 93F693A6 CRC32;

Query Match   79.4%; Score 54; DB 3; Length 251;
Best Local Similarity   57.1%; Pred. No. 1.06e+01;
Matches   4; Conservative   3; Mismatches   0; Indels   0; Gaps   0;

Db   235 DEFVSYY 241
              ::|||:||
Qy   101 EDFVAYY 107

RESULT 9
ID   Q13217   PRELIMINARY;   PRT;   504 AA.
AC   Q13217;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   PROTEIN KINASE INHIBITOR P58.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96235132.
RA   KORTH M.J., LYONS C.N., WAMBACH M., KATZE M.G.;
RL   GENE 170:181-188(1996).
DR   EMBL; U28424; G1353270; -.
DR   PFAM; PF00226; DnaJ.
DR   PFAM; PF00515; TPR.
SQ   SEQUENCE   504 AA;   57580 MW; 86270C88 CRC32;

Query Match   79.4%; Score 54; DB 4; Length 504;
Best Local Similarity   33.3%; Pred. No. 1.06e+01;
Matches   3; Conservative   6; Mismatches   0; Indels   0; Gaps   0;

Db   67 DPDNYIAYY 75
              ::::::|||
Qy   99 ESEDFVAYY 107

RESULT 10
ID   Q60873   PRELIMINARY;   PRT;   504 AA.
AC   Q60873;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   PROTEIN KINASE, INTERFERON INDUCIBLE DOUBLE STRANDED RNA
DE   (PROTEIN KINASE INHIBITOR P58).
GN   PRKRI.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96235132.
RA   KORTH M.J., LYONS C.N., WAMBACH M., KATZE M.G.;
RL   GENE 170:181-188(1996).
DR   EMBL; U28423; G1353272; -.
DR   MGD; MGI:107373; PRKRI.
DR   PFAM; PF00226; DnaJ.
DR   PFAM; PF00515; TPR.
SQ   SEQUENCE   504 AA;   57666 MW; 89862747 CRC32;

Query Match   79.4%; Score 54; DB 11; Length 504;
Best Local Similarity   33.3%; Pred. No. 1.06e+01;
Matches   3; Conservative   6; Mismatches   0; Indels   0; Gaps   0;

Db   67 DPDNYIAYY 75
              ::::::|||
Qy   99 ESEDFVAYY 107

RESULT 11
ID   Q27968   PRELIMINARY;   PRT;   504 AA.
AC   Q27968;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   PKR INHIBITOR P58.
OS   BOS TAURUS (BOVINE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; ARTIODACTYLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94187704.
RA   LEE T.G., TANG N., THOMPSON S., MILLER J., KATZE M.G.;
RL   MOL. CELL. BIOL. 14:2331-2342(1994).
DR   EMBL; U04631; G468012; -.
DR   PFAM; PF00226; DnaJ.
DR   PFAM; PF00515; TPR.
KW   PROTEIN KINASE.
SQ   SEQUENCE   504 AA;   57704 MW; 0DB8EEF4 CRC32;

Query Match   79.4%; Score 54; DB 6; Length 504;
Best Local Similarity   33.3%; Pred. No. 1.06e+01;
Matches   3; Conservative   6; Mismatches   0; Indels   0; Gaps   0;

Db   67 DPDNYIAYY 75
              ::::::|||
Qy   99 ESEDFVAYY 107

RESULT 12
ID   Q61588   PRELIMINARY;   PRT;   81 AA.
AC   Q61588;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)

```
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   G8 (ANTI-MRBC HYBRIDOMA) LIGHT CHAIN.
GN   G8.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NZB;
RX   MEDLINE; 92185208.
RA   CAULFIELD M.J., STANKO D.;
RL   J. IMMUNOL. 148:2068-2073(1992).
DR   EMBL; X60425; E41199; -.
DR   PFAM; PF00047; ig.
SQ   SEQUENCE    81 AA;   8945 MW;  5AF33092 CRC32;

Db   56 QSEDFGSYY 64
         :||||:||
Qy   99 ESEDFVAYY 107

Query Match            77.9%;  Score 53;  DB 11;  Length 81;
Best Local Similarity  66.7%;  Pred. No. 1.60e+01;
Matches    6;  Conservative    2;  Mismatches    1;  Indels   0;  Gaps   0;


RESULT 13
ID   Q16078                     PRELIMINARY;   PRT;   93 AA.
AC   Q16078;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   RF-V KAPPA 1=RHEUMATOID FACTOR V KAPPA REGION (CLONE SLKV7)
DE   (FRAGMENT).
GN   RF-V<KAPPA>1.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94033036.
RA   MARTIN T., CROUZIER R., BLAISON G., LEVALLOIS H., PASQUALI J.L.;
RL   AUTOIMMUNITY 15:163-170(1993).
DR   EMBL; S67060; E98154; -.
DR   PFAM; PF00047; ig.
FT   NON_TER      1      1
FT   NON_TER     93     93
SQ   SEQUENCE    93 AA;   10178 MW;  610E33C1 CRC32;

Db   64 QPEDFATYY 72
         :||| :||
Qy   99 ESEDFVAYY 107

Query Match            77.9%;  Score 53;  DB 4;  Length 93;
Best Local Similarity  55.6%;  Pred. No. 1.60e+01;
Matches    5;  Conservative    3;  Mismatches    1;  Indels   0;  Gaps   0;


RESULT 14
ID   Q16079                     PRELIMINARY;   PRT;   94 AA.
AC   Q16079;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   RF-V KAPPA 1=RHEUMATOID FACTOR V KAPPA REGION (CLONE BKV42)
DE   (FRAGMENT).
GN   RF-V<KAPPA>1.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94033036.
RA   MARTIN T., CROUZIER R., BLAISON G., LEVALLOIS H., PASQUALI J.L.;
RL   AUTOIMMUNITY 15:163-170(1993).
DR   EMBL; S67061; E98155; -.
DR   PFAM; PF00047; ig.
FT   NON_TER      1      1
FT   NON_TER     94     94
SQ   SEQUENCE    94 AA;   10360 MW;  746D2A79 CRC32;

Db   64 QSDDFAVYY 72
         :||:|| ||
Qy   99 ESEDFVAYY 107

Query Match            77.9%;  Score 53;  DB 4;  Length 94;
Best Local Similarity  55.6%;  Pred. No. 1.60e+01;
Matches    5;  Conservative    2;  Mismatches    2;  Indels   0;  Gaps   0;


RESULT 15
ID   Q99514                     PRELIMINARY;   PRT;   105 AA.
AC   Q99514;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   LIGHT CHAIN FAB FRAGMENT (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   HORN M.P., VOGEL M., BIAGGI C., MIESCHER S.M., STADLER B.M.;
RL   SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; Y08148; E274854; -.
DR   PFAM; PF00047; ig.
FT   NON_TER      1      1
FT   NON_TER    105    105
SQ   SEQUENCE   105 AA;   11303 MW;  249B7EC3 CRC32;

Db   77 QPEDFATYY 85
         :||| :||
Qy   99 ESEDFVAYY 107

Query Match            77.9%;  Score 53;  DB 4;  Length 105;
Best Local Similarity  55.6%;  Pred. No. 1.60e+01;
Matches    5;  Conservative    3;  Mismatches    1;  Indels   0;  Gaps   0;


Search completed: Tue Apr 20 14:00:47 1999
Job time : 37 secs.
```

MPSRCH (TM)

```
*****************************************************************************
*****************************************************************************
```

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

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...on: Tue Apr 20 14:08:23 1999; MasPar time 2.95 Seconds
                                   -114.088 Million cell updates/sec
Tabular output not generated.

```
*****************************************************************************
*****************************************************************************
```

Title:
Description: >US-08-836-455-1_1
Perfect Score: (89-97) from trans.pep (3 of 3)
Sequence: 54
                  1 SDYSLTISS 9

Scoring table: PAM 150
                  Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0%
                  Listing first 45 summaries

Database: pir58
                  1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 22.382; Variance 27.684; scale 0.808

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Match	Length	DB	ID	Description	Pred. No.
1	54	100.0	88	2	PL0261	Ig kappa chain V regi	4.80e-01
2	54	100.0	98	2	PH1062	Ig light chain V regi	4.80e-01
3	54	100.0	106	2	PL0260	Ig kappa chain V regi	4.80e-01
4	54	100.0	106	2	PL0259	Ig kappa chain V regi	4.80e-01
5	54	100.0	106	2	PL0262	Ig kappa chain V regi	4.80e-01
6	54	100.0	106	2	B47271	nitrophenyl phosphona	4.80e-01
7	54	100.0	108	4	B23986	Ig kappa chain precur	4.80e-01
8	54	100.0	129	2	D32513	Ig kappa chain precur	4.80e-01
9	54	100.0	130	1	KVMSM4	Ig kappa chain precur	4.80e-01
10	54	100.0	75	2	A34966	Ig heavy chain V regi	4.80e-01
11	54	92.6	98	2	PH1065	Ig kappa chain V regi	3.42e+00
12	54	92.6	101	2	S13701	Ig kappa chain V regi	3.42e+00
13	54	92.6	101	2	S13700	Ig kappa chain V regi	3.42e+00
14	54	92.6	101	2	C28840	Ig kappa chain V regi	3.42e+00
15	54	92.6	101	2	B28840	Ig kappa chain V regi	3.42e+00
16	54	92.6	103	2	S13703	Ig kappa chain V regi	3.42e+00
17	54	92.6	104	2	S13700	Ig kappa chain V regi	3.42e+00
18	54	92.6	115	1	KVMSL6	Ig kappa chain precur	3.42e+00
19	50	92.6	117	2	S21668	Ig kappa chain V regi	3.42e+00
20	50	92.6	117	2	S41814	Ig kappa chain V regi	3.42e+00
21	50	92.6	120	2	S21666	Ig kappa chain V regi	3.42e+00
22	50	92.6	120	2	S21667	Ig kappa chain V regi	3.42e+00
23	50	92.6	127	2	S52447	Ig kappa chain V regi	3.42e+00
24	50	92.6	152	2	S30751	Ig kappa chain precur	3.42e+00
25	50	92.6	234	2	S14237	Ig kappa chain precur	3.42e+00
26	49	90.7	105	2	PH0087	Ig kappa chain V regi	5.51e+00
27	49	90.7	107	2	B28044	Ig kappa chain V regi	5.51e+00
28	49	90.7	107	2	S69901	Ig kappa chain (clone	5.51e+00
29	49	90.7	107	2	S33188	Ig kappa chain V regi	5.51e+00
30	49	90.7	107	2	B49026	Ig kappa chain V regi	5.51e+00
31	49	90.7	108	2	S11124	Ig kappa chain V regi	5.51e+00
32	49	90.7	108	2	C26405	Ig kappa chain V regi	5.51e+00
33	49	90.7	108	2	B26405	Ig kappa chain V regi	5.51e+00
34	49	90.7	108	2	B30551	Ig kappa chain (clone	5.51e+00
35	49	90.7	108	2	S69902	Ig kappa chain V regi	5.51e+00
36	49	90.7	108	2	S59903	Ig kappa chain (clone	5.51e+00
37	49	90.7	109	2	S38862	Ig kappa chain V regi	5.51e+00
38	49	90.7	108	2	PH0088	Ig kappa chain V regi	5.51e+00
39	49	90.7	111	2	A38740	Ig kappa chain precur	5.51e+00
40	49	90.7	111	2	C38740	Ig kappa chain V regi	5.51e+00
41	49	90.7	115	2	A53276	Ig kappa chain V regi	5.51e+00
42	49	90.7	115	2	C24405	Ig kappa chain V regi	5.51e+00
43	49	90.7	122	2	A29380	Ig kappa chain precur	5.51e+00
44	49	90.7	122	2	PL0101	Ig kappa chain precur	5.51e+00
45	49	90.7	128	2	A26406	Ig kappa chain V regi	5.51e+00

ALIGNMENTS

RESULT   1

ENTRY   PL0261   #type fragment
TITLE   Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
               09-May-1997
ACCESSIONS   PL0261
REFERENCE   PL0231
               #authors Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
               D.; Marshak-Rothstein, A.; Weigert, M.
               #journal J. Exp. Med. (1990) 171:265-297
               #title Anti-DNA antibodies from autoimmune mice arise by clonal
               expansion and somatic mutation.
               #cross-references MUID:90111618
               #accession PL0261
               ##molecule_type mRNA
               ##residues 1-88 ##label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
FEATURE
               1-5   #region framework 1\
               6-16   #region complementarity-determining 1\
               17-31 #region framework 2\
               32-38 #region complementarity-determining 2\
               39-70 #region framework 3\
               71-79 #region complementarity-determining 3\
               80-88 #region framework 4
SUMMARY   #length 88 #checksum 7092

Query Match   100.0%; Score 54; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.80e-01;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   89 SDYSLTISS 97
         |||||||||
Db   51 SDYSLTISS 59

RESULT   2

ENTRY   S17622   #type complete
TITLE   Ig kappa chain V region - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
               09-May-1997
ACCESSIONS   S17622
REFERENCE   S17230
               #authors Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

#journal   Nature (1991) 352:624-628 ---
#title   Making antibody fragments using phage display libraries.
#cross-references MUID:91326098
#accession   S17622
##status   preliminary
##molecule_type nucleic acid
##residues   1-91 ##label C1A
CLASSIFICATION
KEYWORDS   #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY   heterotetramer; immunoglobulin
              #length 91 #molecular-weight 9895 #checksum 3446

Query Match   100.0%;   Score 54; DB 2; Length 91;
Best Local Similarity 100.0%;   Pred. No. 4.80e-01;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db 61 SDYSLTISS 69
        |||||||||
Qy 89 SDYSLTISS 97

RESULT 3
ENTRY   PH1062   #type fragment
TITLE   Ig light chain V region (clone 202.105) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
              15-Jun-1996
ACCESSIONS   PH1062
REFERENCE   PH0971
              Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
#authors
#journal   J. Exp. Med. (1992) 176:761-779
#title   Both IgM and IgG anti-DNA antibodies are the products of
              clonally selective B cell stimulation in (NZB x NZW)F1
              mice.
#accession   PH1062
##status   nucleic acid sequence not shown
##molecule_type mRNA
##residues   1-98 ##label TIL
##experimental_source B cell, strain [NZB x NZW]F1
CLASSIFICATION
KEYWORDS   #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY   immunoglobulin
              #length 98 #checksum 6933

Query Match   100.0%;   Score 54; DB 2; Length 98;
Best Local Similarity 100.0%;   Pred. No. 4.80e-01;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db 69 SDYSLTISS 77
        |||||||||
Qy 89 SDYSLTISS 97

RESULT 4
ENTRY   PL0260   #type fragment
TITLE   Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
              16-Aug-1996
ACCESSIONS   PL0260
REFERENCE   PL0231
              Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
#authors   D.; Marshak-Rothstein, A.; Weigert, M.
#journal   J. Exp. Med. (1990) 171:265-297
#title   Anti-DNA antibodies from autoimmune mice arise by clonal
              expansion and somatic mutation.
#cross-references MUID:90111618
#accession   PL0260
##molecule_type mRNA
##residues   1-106 ##label SHL
CLASSIFICATION
KEYWORDS   #superfamily immunoglobulin V region; immunoglobulin homology
              heterotetramer; immunoglobulin
FEATURE
1-23   #region framework 1\
24-34   #region complementarity-determining 1\

SUMMARY
              35-49   #region framework 2\
              50-56   #region complementarity-determining 2\
              57-88   #region framework 3\
              89-97   #region complementarity-determining 3\
              98-106   #region framework 4
              #length 106 #checksum 2157

Query Match   100.0%;   Score 54; DB 2; Length 106;
Best Local Similarity 100.0%;   Pred. No. 4.80e-01;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db 69 SDYSLTISS 77
        |||||||||
Qy 89 SDYSLTISS 97

RESULT 5
ENTRY   PL0259   #type fragment
TITLE   Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
              16-Aug-1996
ACCESSIONS   PL0259
REFERENCE   PL0231
              Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
#authors   D.; Marshak-Rothstein, A.; Weigert, M.
#journal   J. Exp. Med. (1990) 171:265-297
#title   Anti-DNA antibodies from autoimmune mice arise by clonal
              expansion and somatic mutation.
#cross-references MUID:90111618
#accession   PL0259
##molecule_type mRNA
##residues   1-106 ##label SHL
CLASSIFICATION
KEYWORDS   #superfamily immunoglobulin V region; immunoglobulin homology
              heterotetramer; immunoglobulin
FEATURE
1-23   #region framework 1\
24-34   #region complementarity-determining 1\
35-49   #region framework 2\
50-56   #region complementarity-determining 2\
57-88   #region framework 3\
89-97   #region complementarity-determining 3\
98-106   #region framework 4
              #length 106 #checksum 2162

Query Match   100.0%;   Score 54; DB 2; Length 106;
Best Local Similarity 100.0%;   Pred. No. 4.80e-01;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db 69 SDYSLTISS 77
        |||||||||
Qy 89 SDYSLTISS 97

RESULT 6
ENTRY   PL0262   #type fragment
TITLE   Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
              16-Aug-1996
ACCESSIONS   PL0262
REFERENCE   PL0231
              Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
#authors   D.; Marshak-Rothstein, A.; Weigert, M.
#journal   J. Exp. Med. (1990) 171:265-297
#title   Anti-DNA antibodies from autoimmune mice arise by clonal
              expansion and somatic mutation.
#cross-references MUID:90111618
#accession   PL0262
##molecule_type mRNA
##residues   1-106 ##label SHL
CLASSIFICATION
KEYWORDS   #superfamily immunoglobulin V region; immunoglobulin homology
              heterotetramer; immunoglobulin

FEATURE
 1-23 #region framework 1\
 24-34 #region complementarity-determining 1\
 35-49 #region framework 2\
 50-56 #region complementarity-determining 2\
 57-88 #region framework 3\
 89-97 #region complementarity-determining 3\
 98-106 #region framework 4\
SUMMARY #length 106 #checksum 658

```
Qy  89 SDYSLTISS 97
       |||||||||
Db  69 SDYSLTISS 77
```

Query Match 100.0%; Score 54; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.80e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
ENTRY
TITLE B47271 #type fragment
 nitrophenyl phosphonate-specific antibody 48G7 light chain VJ
 - synthetic (fragment)
ORGANISM #formal_name synthetic
#note Mus musculus (house mouse) gene engineered and expressed in
 Escherichia coli
DATE 21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change
ACCESSIONS B47271
REFERENCE B47271
#authors Lesley, S.A.; Patten, P.A.; Schultz, P.G.
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1160-1165
#title A genetic approach to the generation of antibodies with
 enhanced catalytic activities.
#cross-references MUID:93165660
##accession B47271
##molecule_type DNA; protein
##residues 1-108 ##label LES
##note sequence extracted from NCBI backbone (NCBIN:124856,
 NCBIP:124859)
##note parts of this sequence were determined by protein
 sequencing

FEATURE
 24-89 #disulfide_bonds #status predicted
SUMMARY #length 108 #checksum 9036

```
Qy  89 SDYSLTISS 97
       |||||||||
Db  70 SDYSLTISS 78
```

Query Match 100.0%; Score 54; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.80e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
ENTRY B23986 #type complete
TITLE Ig kappa chain precursor V region (IR2) - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change
ACCESSIONS B23986
REFERENCE A91541
#authors Hellman, L.; Engstrom, A.; Bennich, H.; Pettersson, U.
#journal Gene (1985) 40:107-114
#title Structure and expression of kappa-chain genes in two
 IgE-producing rat immunocytomas.
#cross-references MUID:86137406
##accession B23986
##molecule_type mRNA
##residues 1-129 ##label HEL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; Immunoglobulin

SUMMARY #length 129 #molecular-weight 14217 #checksum 5336

```
Qy  89 SDYSLTISS 97
       |||||||||
Db  91 SDYSLTISS 99
```

Query Match 100.0%; Score 54; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 4.80e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
ENTRY D32513 #type complete
TITLE Ig kappa chain precursor V region (BXW16) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 21-May-1990 #sequence_revision 31-Dec-1990 #text_change
ACCESSIONS D32513
REFERENCE A94689
#authors Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.;
 Noonan, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos,
 A.N.
#journal J. Clin. Invest. (1988) 82:852-860
#title Immunoglobulin kappa light chain variable region gene complex
 organization and immunoglobulin genes encoding anti-DNA
 autoantibodies in lupus mice.
#cross-references MUID:88331394
##accession D32513
##molecule_type DNA
##residues 1-129 ##label KOF
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 129 #molecular-weight 14097 #checksum 3457

```
Qy  89 SDYSLTISS 97
       |||||||||
Db  91 SDYSLTISS 99
```

Query Match 100.0%; Score 54; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 4.80e-01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
ENTRY KVMSM4 #type complete
TITLE Ig kappa chain precursor V region (MOPC 41) - mouse
CONTAINS Ig kappa chain precursor V region VK41
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change
ACCESSIONS A93211; B93211; A93815; A94239; A01922; A01923
REFERENCE A93211
#authors Seidman, J.G.; Max, E.E.; Leder, P.
#journal Nature (1979) 280:370-375
#title A kappa-immunoglobulin gene is formed by site-specific
 recombination without further somatic mutation.
#cross-references MUID:79221900
##accession A93211
##residues 1-130 ##label PC41
##molecule_type DNA
##residues 1-117 ##label VK41
##note the sequences were determined from the differentiated
 gene MOPC 41 and the germline gene VK41
REFERENCE A93815
#authors Burstein, Y.; Schechter, I.
#journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720
#title Amino acid sequence of the NH-2-terminal extra piece
 of the precursors of mouse immunoglobulin lambda-1-type and
 kappa-type light chains.
#cross-references MUID:77148916

#accession A93815
##molecule_type protein
##residues 1-33 ##label BUR
##note Met-3 is apparently used as an alternative initiator in 258 of the chains

REFERENCE
#authors Gray, W.R.; Dreyer, W.J.; Hood, L.
#journal Science (1967) 155:465-467
#title Mechanism of antibody synthesis: size differences between mouse kappa chains.
#cross-references MUID:67056897
#accession A94239
##molecule_type protein
##residues 23-49,'B',51-53,'LSB',57-58,'ZZ',61-62,'Bz',65-76,'B', 78-108,110-130 ##label GRA
##experimental_source Bence Jones protein MOPC 41

GENETICS
1PLEX
#introns 19/1

An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS alternative initiators; heterotetramer; immunoglobulin
FEATURE
1-22 #domain signal sequence #status experimental #label SIG1\
3-22 #domain signal sequence #status experimental #label SIG2\
23-130 #product Ig kappa chain V region (MOPC 41) #status experimental #label M41\
38-112 #domain immunoglobulin homology #label IMM\
45-110 #disulfide_bonds #status predicted
SUMMARY #length 130 #molecular-weight 14311 #checksum 6707

Query Match
Best Local Similarity 100.0%;   Score 54; DB 1; Length 130;
Matches 9; Conservative 0; Pred. No. 4.80e-01; Mismatches 0; Indels 0; Gaps 0;

Db 91 SDYSLTISS 99
        |||||||||
Qy 89 SDYSLTISS 97

RESULT 11
ENTRY A34966 #type fragment
TITLE Ig heavy chain V region (PR8-9) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 08-Sep-1997
ACCESSIONS A34966
REFERENCE A36025
#authors Caton, A.J.; Koprowski, H.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6450-6454
#title Influenza virus hemagglutinin-specific antibodies isolated from a combinatorial expression library are closely related to the immune response of the donor.
#cross-references MUID:90349634
#accession A34966
##status preliminary
##molecule_type mRNA
##residues 1-75 ##label CAT
##cross-references GB:M57280; NID:g197784; PID:g197785
##superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 75 #checksum 1748

CLASSIFICATION
KEYWORDS heterotetramer; immunoglobulin

Query Match   92.6%;
Best Local Similarity 100.0%;   Score 50; DB 2; Length 75;
Matches 8; Conservative 0; Pred. No. 3.42e+00; Mismatches 0; Indels 0; Gaps 0;

Db 41 DYSLTISS 48
        ||||||||
Qy 90 DYSLTISS 97

RESULT 12
ENTRY PH1065 #type fragment
TITLE Ig kappa chain V region (clone 163.47) - mouse (fragment)
#molecule_type mRNA
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Feb-1998
ACCESSIONS PH1065
REFERENCE PH0971
#authors Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
#journal J. Exp. Med. (1992) 176:761-779
#title Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice.
#accession PH1065
##status nucleic acid sequence not shown
##molecule_type mRNA
##residues 1-98 ##label TIL
##experimental_source B cell, strain [NZB x NZW]F1
CLASSIFICATION
KEYWORDS #superfamily immunoglobulin V region; immunoglobulin homology
immunoglobulin
SUMMARY #length 98 #checksum 4553

Query Match
Best Local Similarity 100.0%;   Score 50; DB 2; Length 98;
Matches 8; Conservative 0; Pred. No. 3.42e+00; Mismatches 0; Indels 0; Gaps 0;

Db 70 DYSLTISS 77
        ||||||||
Qy 90 DYSLTISS 97

RESULT 13
ENTRY S13701 #type fragment
TITLE Ig kappa chain V region (hybridoma NC19-E11) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
#accession S13701
##status preliminary
##molecule_type mRNA
##residues 1-101 ##label PEN
##cross-references EMBL:X53354
##superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 101 #checksum 6598
ACCESSIONS S13701
REFERENCE S13685
#authors Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
#journal Eur. J. Immunol. (1989) 19:1289-1295
#title Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clonal selection.
#cross-references MUID:89338557
CLASSIFICATION
KEYWORDS immunoglobulin
SUMMARY

Query Match   92.6%;
Best Local Similarity 100.0%;   Score 50; DB 2; Length 101;
Matches 8; Conservative 0; Pred. No. 3.42e+00; Mismatches 0; Indels 0; Gaps 0;

Db 70 DYSLTISS 77
        ||||||||
Qy 90 DYSLTISS 97

RESULT 14
ENTRY C28840 #type fragment
TITLE Ig kappa chain V region (HP22) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse

```
DATE          29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change
              16-Aug-1996
ACCESSIONS    C28840; J25114
REFERENCE     A91028
  #authors    Oller, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau,
              M.
  #journal    EMBO J. (1985) 4:3681-3688
  #title      The idiotypic network and the internal image: possible
              regulation of a germ-line network by paucigene encoded Ab2
              (anti-idiotypic) antibodies in the GAT system.
  #cross-references MUID:86136012
  #accession  C28840
    ##molecule_type mRNA
    ##residues 1-101 ##label OLL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
SUMMARY       #length 101 #checksum 5983

Query Match               92.6%;  Score 50;  DB 2;  Length 101;
Best Local Similarity 100.0%;   Pred. No. 3.42e+00;
  Matches     8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db     64 DYSLTISS 71
          ||||||||
Qy     90 DYSLTISS 97


RESULT 15
ENTRY     B28840       #type fragment
TITLE     Ig kappa chain V region (HP27) - mouse (fragment)
ORGANISM  #formal_name Mus musculus #common_name house mouse
DATE      29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change
          16-Aug-1996
ACCESSIONS B28840; I25114
REFERENCE  A91028
  #authors Oller, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau,
           M.
  #journal EMBO J. (1985) 4:3681-3688
  #title   The idiotypic network and the internal image: possible
           regulation of a germ-line network by paucigene encoded Ab2
           (anti-idiotypic) antibodies in the GAT system.
  #cross-references MUID:86136012
  #accession B28840
    ##molecule_type mRNA
    ##residues 1-101 ##label OLL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY    #length 101 #checksum 7015

Query Match               92.6%;  Score 50;  DB 2;  Length 101;
Best Local Similarity 100.0%;   Pred. No. 3.42e+00;
  Matches     8;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db     64 DYSLTISS 71
          ||||||||
Qy     90 DYSLTISS 97


Search completed: Tue Apr 20 14:08:41 1999
Job time : 18 secs.
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                    MPSRCH (TM)

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```

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

on on: Tue Apr 20 14:07:20 1999; MasPar time 2.27 Seconds
Tabular output not generated.   106.236 Million cell updates/sec

Title:	
Description:	>US-08-836-455-1_1
Perfect Score:	(89-97) from trans.pep (3 of 3)
Sequence:	54
	1 SDYSLTISS 9
Scoring table:	PAM 150
	Gap 11
Searched:	74019 seqs, 26840295 residues
Post-processing:	Minimum Match 0%
	Listing first 45 summaries
Database:	swiss-prot35
	1:swissprot
Statistics:	Mean 22.743; Variance 22.907; scale 0.993

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID		Description	Pred. No.
1	54	100.0	130	1	KV5G_MOUSE	IG KAPPA CHAIN PRECURS	4.31e-02
2	50	92.6	115	1	KV5F_MOUSE	IG KAPPA CHAIN PRECURS	4.56e-01
3	49	90.7	108	1	KV5K_MOUSE	IG KAPPA CHAIN V-V REG	8.08e-01
4	49	90.7	108	1	KV5J_MOUSE	IG KAPPA CHAIN V-V REG	8.08e-01
5	49	90.7	108	1	KV5N_MOUSE	IG KAPPA CHAIN V-V REG	8.08e-01
6	49	90.7	108	1	KV5O_MOUSE	IG KAPPA CHAIN V-V REG	8.08e-01
7	49	90.7	108	1	KV5L_MOUSE	IG KAPPA CHAIN V-V REG	8.08e-01
8	49	90.7	108	1	KV5M_MOUSE	IG KAPPA CHAIN V-V REG	8.08e-01
9	47	87.0	108	1	KV5U_MOUSE	IG KAPPA CHAIN V-V REG	2.47e+00
10	47	87.0	435	1	YT13_CAEEL	HYPOTHETICAL 48.6 KD P	2.47e+00
11	47	87.0	558	1	TCPH_SCHPO	PROBABLE T-COMPLEX PRO	2.47e+00
12	46	85.2	107	1	KV6C_MOUSE	IG KAPPA CHAIN V-VI RE	4.26e+00
13	46	85.2	107	1	KV6D_MOUSE	IG KAPPA CHAIN V-VI RE	4.26e+00
14	46	85.2	107	1	KV6A_MOUSE	IG KAPPA CHAIN V-VI RE	4.26e+00
15	46	85.2	107	1	KV6B_MOUSE	IG KAPPA CHAIN V-VI RE	4.26e+00
16	46	85.2	110	1	KV13_RABIT	IG KAPPA CHAIN V REGIO	4.26e+00
17	46	85.2	117	1	KV5H_MOUSE	IG KAPPA CHAIN V-V REG	4.26e+00
18	46	85.2	129	1	KV4A_MOUSE	IG KAPPA CHAIN PRECURS	4.26e+00
19	46	85.2	107	1	KV1D_HUMAN	IG KAPPA CHAIN V-I REG	4.26e+00
20	45	83.3	108	1	KV5T_MOUSE	IG KAPPA CHAIN V-V REG	7.28e+00
21	45	83.3	108	1	KV1H_HUMAN	IG KAPPA CHAIN V-I REG	7.28e+00
22	45	83.3	108	1	KV5R_MOUSE	IG KAPPA CHAIN V-V REG	7.28e+00
23	45	83.3	108	1	KV5Q_MOUSE	IG KAPPA CHAIN V-V REG	7.28e+00
24	45	83.3	108	1	KV5S_MOUSE	IG KAPPA CHAIN V-V REG	7.28e+00
25	45	83.3	109	1	KV1T_HUMAN	IG KAPPA CHAIN V-I REG	7.28e+00
26	45	83.3	114	1	KV1A_MOUSE	IG KAPPA CHAIN V-I REG	7.28e+00
27	45	83.3	114	1	KV4A_HUMAN	IG KAPPA CHAIN V-IV RE	7.28e+00
28	45	83.3	115	1	KV3I_HUMAN	IG KAPPA CHAIN V-III R	7.28e+00
29	45	83.3	116	1	KV3J_HUMAN	IG KAPPA CHAIN PRECURS	7.28e+00
30	45	83.3	117	1	KV1I_HUMAN	IG KAPPA CHAIN PRECURS	7.28e+00
31	45	83.3	121	1	KV4O_HUMAN	IG KAPPA CHAIN PRECURS	7.28e+00
32	45	83.3	128	1	KV5E_MOUSE	IG KAPPA CHAIN PRECURS	7.28e+00
33	45	83.3	129	1	KV1W_HUMAN	IG KAPPA CHAIN V-I REG	7.28e+00
34	45	83.3	134	1	KV4B_HUMAN	IG KAPPA CHAIN PRECURS	7.28e+00
35	45	83.3	136	1	KV4C_HUMAN	IG KAPPA CHAIN PRECURS	7.28e+00
36	44	81.5	136	1	KV5B_MOUSE	IG KAPPA CHAIN V-VI RE	1.23e+01
37	44	81.5	107	1	KV6G_MOUSE	IG KAPPA CHAIN V-VI RE	1.23e+01
38	44	81.5	107	1	KV6J_MOUSE	IG KAPPA CHAIN V-VI RE	1.23e+01
39	44	81.5	107	1	KV6I_MOUSE	IG KAPPA CHAIN V-VI RE	1.23e+01
40	44	81.5	107	1	KV6H_MOUSE	IG KAPPA CHAIN V-VI RE	1.23e+01
41	44	81.5	107	1	KV6F_MOUSE	IG KAPPA CHAIN V-VI RE	1.23e+01
42	44	81.5	108	1	KV1G_HUMAN	IG KAPPA CHAIN V-I REG	1.23e+01
43	44	81.5	108	1	KV1F_HUMAN	IG KAPPA CHAIN V-I REG	1.23e+01
44	44	81.5	108	1	KV1S_HUMAN	IG KAPPA CHAIN V-I REG	1.23e+01
45	44	81.5	109	1	KV3F_HUMAN	IG KAPPA CHAIN V-III R	1.23e+01

ALIGNMENTS

```
RESULT  1
ID   KV5G_MOUSE     STANDARD;      PRT;   130 AA.
AC   P01639; P01640;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 41).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 79221900.
RA   SEIDMAN J.G.; MAX E.E.; LEDER P.;
RL   NATURE 280:370-375(1979).
RN   [2]
RP   SEQUENCE OF 1-33.
RX   MEDLINE; 77148916.
RA   BURSTEIN Y., SCHECHTER I.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 74:716-720(1977).
RN   [3]
RP   SEQUENCE OF 23-130.
RX   MEDLINE; 67056897.
RA   GRAY W.R.; DREYER W.J.; HOOD L.;
RL   SCIENCE 155:465-467(1967).
CC   -!- THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE SYSTEM DIRECTED BY
CC       MRNA ISOLATED FROM MYELOMA POLYSOMES.
CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01922; KVMSM4.
     HSSP; P01607; 6FAB.
KW   IMMUNOGLOBULIN V REGION; SIGNAL; BENCE-JONES PROTEIN.
FT   SIGNAL         1     22
FT   CHAIN         23    130    IG KAPPA CHAIN V-V REGION (MOPC 41).
FT   DOMAIN        23     45    FRAMEWORK 1.
FT   DOMAIN        46     56    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        57     71    FRAMEWORK 2.
FT   DOMAIN        72     78    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        79    110    FRAMEWORK 3.
FT   DOMAIN       111    119    COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       120    129    FRAMEWORK 4.
FT   VARIANT        1      1    MISSING (IN 25% OF THE MOLECULES).
FT   DISULFID      45    110    BY SIMILARITY.
FT   NON_TER        1      1
SQ   SEQUENCE   130 AA;   14311 MW;   E77D75A2 CRC32;
```

Query Match   100.0%;   Score 54;   DB 1;   Length 130;
Best Local Similarity 100.0%;   Pred. No. 4.31e-02;

```
Matches     9;  Conservative     0;  Mismatches     0;  Indels     0;  Gaps     0;

Db    91  SDYSLTISS  99
          |||||||||
Qy    89  SDYSLTISS  97

RESULT 2
ID   KV5F_MOUSE     STANDARD;      PRT;   115 AA.
AC   P01638;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-V REGION (L6) (FRAGMENT).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
     [1]
RL   SEQUENCE FROM N.A.
     MEDLINE; 81220975.
     PECH M., HOCHTL J., SCHNELL H., ZACHAU H.G.;
RL   NATURE 291:668-670(1981).
DR   PIR; A01921; KVMSL6.
     HSSP; P01607; 1IIF.
KW   IMMUNOGLOBULIN V REGION; SIGNAL.
FT   SIGNAL       1      20
FT   CHAIN       21    >115
FT   DOMAIN      21     115    IG KAPPA CHAIN V-V REGION (L6).
FT   DOMAIN      21      43    FRAMEWORK-1.
FT   DOMAIN      44      54    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      55      69    FRAMEWORK 2.
FT   DOMAIN      70      76    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      77     108    FRAMEWORK 3.
FT   DOMAIN     109    >115    COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID    43     108    BY SIMILARITY.
FT   NON_TER    115     115
SQ   SEQUENCE   115 AA;   12986 MW;   958689AF CRC32;

Query Match             92.6%;  Score  50;  DB 1;  Length 115;
Best Local Similarity  100.0%;  Pred. No. 4.56e-01;
Matches     8;  Conservative     0;  Mismatches     0;  Indels     0;  Gaps     0;

Db    90  DYSLTISS  97
          ||||||||
Qy    90  DYSLTISS  97

LT 3
ID   KV5K_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01644;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP R16.7).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
     [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
     MEDLINE; 82150934.
     SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
     PIR; A01927; KVMSAR.
     HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN       1      23    FRAMEWORK 1.
FT   DOMAIN      24      34    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      35      49    FRAMEWORK 2.
FT   DOMAIN      50      56    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      57      88    FRAMEWORK 3.
FT   DOMAIN      89      97    COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      98     108    FRAMEWORK 4.
```

```
FT   DISULFID    23      88    BY SIMILARITY.
FT   NON_TER    108     108
SQ   SEQUENCE   108 AA;   11910 MW;   64A62905 CRC32;

Query Match             90.7%;  Score  49;  DB 1;  Length 108;
Best Local Similarity   77.8%;  Pred. No. 8.08e-01;
Matches     7;  Conservative     2;  Mismatches     0;  Indels     0;  Gaps     0;

Db    69  TDYSLTISN  77
          ||||||||:
Qy    89  SDYSLTISS  97

RESULT 4
ID   KV5J_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01643;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (MOPC 173).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
     [1]
     SEQUENCE.
     MEDLINE; 76091934.
RA   SCHIFF C., FOUGEREAU M.;
RL   EUR. J. BIOCHEM. 59:525-537(1975).
CC   -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01926; KVMS73.
     HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION.
FT   DOMAIN       1      23    FRAMEWORK 1.
FT   DOMAIN      24      34    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      35      49    FRAMEWORK 2.
FT   DOMAIN      50      56    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      57      88    FRAMEWORK 3.
FT   DOMAIN      89      97    COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      98     108    FRAMEWORK 4.
FT   DISULFID    23      88    BY SIMILARITY.
FT   NON_TER    108     108
SQ   SEQUENCE   108 AA;   11819 MW;   EA186054 CRC32;

Query Match             90.7%;  Score  49;  DB 1;  Length 108;
Best Local Similarity   77.8%;  Pred. No. 8.08e-01;
Matches     7;  Conservative     2;  Mismatches     0;  Indels     0;  Gaps     0;

Db    69  TDYSLTISB  77
          ||||||||:
Qy    89  SDYSLTISS  97

RESULT 5
ID   KV5N_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01647;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 124E1).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
     [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
     MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
     PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR   PIR; A01927; KVMSAR.
     HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN       1      23    FRAMEWORK 1.
```

```
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    108       FRAMEWORK 4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE    108 AA;  11965 MW;  84754175 CRC32;

Qy          89 SDYSLTISN 97
               :|||:||||:
Db          69 TDYSLTISN 77

Matches          7; Conservative      2; Mismatches      0; Indels      0; Gaps      0;
Best Local Similarity   77.8%;  Pred. No. 8.08e-01;
Query Similarity   90.7%;  Score 49;  DB 1; Length 108;

RESULT   6
ID   KV5O_MOUSE    STANDARD;    PRT;    108 AA.
AC   P01648;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 91A3).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
PIR; A01927; KVMSAR.
HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN         1     23       FRAMEWORK 1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    108       FRAMEWORK 4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE    108 AA;  11961 MW;  5B067780 CRC32;

Query Match   90.7%;  Score 49;  DB 1; Length 108;
Best Local Similarity   77.8%;  Pred. No. 8.08e-01;
Matches          7; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

Qy          89 SDYSLTISN 97
               :|||:||||:
Db          69 TDYSLTISN 77

RESULT   7
ID   KV5L_MOUSE    STANDARD;    PRT;    108 AA.
AC   P01645;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 93G7).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE; 82150934.
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RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
PIR; A01927; KVMSAR.
HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN         1     23       FRAMEWORK 1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    108       FRAMEWORK 4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE    108 AA;  11954 MW;  A203E130 CRC32;

Qy          89 SDYSLTISN 97
               :|||:||||:
Db          69 TDYSLTISN 77

Matches          7; Conservative      2; Mismatches      0; Indels      0; Gaps      0;
Best Local Similarity   77.8%;  Pred. No. 8.08e-01;
Query Match   90.7%;  Score 49;  DB 1; Length 108;

RESULT   8
ID   KV5M_MOUSE    STANDARD;    PRT;    108 AA.
AC   P01646;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 123E6).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
PIR; A01927; KVMSAR.
HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN         1     23       FRAMEWORK 1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    108       FRAMEWORK 4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE    108 AA;  11989 MW;  23B8BB67 CRC32;

Query Match   90.7%;  Score 49;  DB 1; Length 108;
Best Local Similarity   77.8%;  Pred. No. 8.08e-01;
Matches          7; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

Qy          89 SDYSLTISN 97
               :|||:||||:
Db          69 TDYSLTISN 77

RESULT   9
ID   KV5U_MOUSE    STANDARD;    PRT;    108 AA.
AC   P04946;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (NQ5-89.4).
```

OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 83271467.
RA   KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;
RL   NATURE 304:320-324(1983).
CC   -!- ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
DR   EMBL; K00745; G196455; -.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; HYBRIDOMA.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   107   FRAMEWORK 4.
FT   DISULFID   23   88   BY SIMILARITY.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA; 11866 MW; D396F142 CRC32;

Query Match   87.0%; Score 47; DB 1; Length 108;
Best Local Similarity   66.7%; Pred. No. 2.47e+00;
Matches   6; Conservative   3; Mismatches   0; Indels   0; Gaps   0;

Qy   89 SDYSLTISS 97
              :|||||||::
Db   69 TDYSLTITN 77

RESULT 10
ID   YT13_CAEEL   STANDARD;   PRT;   435 AA.
AC   Q10917;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 48.6 KD PROTEIN B0252.3 IN CHROMOSOME II.
GN   B0252.3.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIDA.
OC   EUKARYOTA; METAZOA; ACOELOMATES; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
DU   2.; WATERSTON R.;
RL   SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
DR   EMBL; U23453; G733576; -.
DR   WORMPEP; B0252.3; CE02419.
KW   HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
FT   TRANSMEM   55   75   POTENTIAL.
FT   TRANSMEM   384   404   POTENTIAL.
SQ   SEQUENCE   435 AA; 48571 MW; C964157F CRC32;

Query Match   87.0%; Score 47; DB 1; Length 435;
Best Local Similarity   87.5%; Pred. No. 2.47e+00;
Matches   7; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   90 DYSLTISS 97
              |||:|||||
Db   13 DYNLTISS 20

RESULT 11
ID   TCPH_SCHPO   STANDARD;   PRT;   558 AA.
AC   P87153;
DT   15-JUL-1998 (REL. 36, CREATED)
DT   15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT   15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE   PROBABLE T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA).
DE   CCT7 OR SPBC25H2.12C.
OS   SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   DURSO G., LYE G., BOWMAN S., CHURCH C., WOOD V., BARRELL B.G.,
RA   RAJANDREAM M.A., CONNOR R.E.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON
CC   ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF
CC   -!- ACTIN AND TUBULIN (BY SIMILARITY).
CC   -!- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 KD THAT
CC   FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC   -!- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
DR   EMBL; Z95397; E315886; -.
DR   PROSITE; PS00750; TCP1_1; 1.
DR   PROSITE; PS00751; TCP1_2; 1.
DR   PROSITE; PS00995; TCP1_3; 1.
KW   CHAPERONE; ATP-BINDING; MULTIGENE FAMILY.
SQ   SEQUENCE   558 AA; 60686 MW; 0A27A3C4 CRC32;

Query Match   87.0%; Score 47; DB 1; Length 558;
Best Local Similarity   87.5%; Pred. No. 2.47e+00;
Matches   7; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   90 DYSLTISS 97
              |||||||:
Db   427 DYSLTISG 434

RESULT 12
ID   KV6C_MOUSE   STANDARD;   PRT;   107 AA.
AC   P01677;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-VI REGION (TEPC 601 AND TEPC 191).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE (TEPC 601).
RX   MEDLINE; 81054757.
RA   RUDIKOFF S., RAO D.N., GLADEMANS C.P.J., POTTER M.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 77:4270-4274(1980).
RN   [2]
RP   SEQUENCE (TEPC 191).
RX   MEDLINE; 79082830.
RA   RAO D.N., RUDIKOFF S., POTTER M.;
RL   BIOCHEMISTRY 17:5555-5559(1978).
CC   -!- THE TWO SEQUENCES ARE IDENTICAL.
CC   -!- THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS THAT BIND
CC   GALACTAN.
DR   PIR; A01941; KVMSX4.
DR   HSSP; P01679; 2FBJ.
KW   IMMUNOGLOBULIN V REGION.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   33   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   34   48   FRAMEWORK 2.
FT   DOMAIN   49   55   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   56   87   FRAMEWORK 3.
FT   DOMAIN   88   96   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   97   106   FRAMEWORK 4.
FT   DISULFID   23   87   BY SIMILARITY.
FT   NON_TER   107   107
SQ   SEQUENCE   107 AA; 11568 MW; 154F6572 CRC32;

Query Match   85.2%; Score 46; DB 1; Length 107;
Best Local Similarity   77.8%; Pred. No. 4.26e+00;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   90 DYSLTISS 97
              ||||||:|
Db   68 TSYSLTISS 76

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Qy     89  SDYSLTISS  97

RESULT   13
ID   KV6D_MOUSE     STANDARD;      PRT;    107 AA.
AC   P01678;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-VI REGION (SAPC 10).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 81054757.
RA   RUDIKOFF S., RAO D.N., GLAUDEMANS C.P.J., POTTER M.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 77:4270-4274(1980).
CC   -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.
     PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ.
     IMMUNOGLOBULIN V REGION.
FT   DOMAIN        1     23      FRAMEWORK 1.
FT   DOMAIN       24     33      COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       34     48      FRAMEWORK 2.
FT   DOMAIN       49     55      COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       56     87      FRAMEWORK 3.
FT   DOMAIN       88     96      COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       97    106      FRAMEWORK 4.
FT   DISULFID     23     87      BY SIMILARITY.
FT   NON_TER     107    107
SQ   SEQUENCE    107 AA;   11554 MW;  609EDE13 CRC32;

Qy     89  SDYSLTISS  97

Db     68  TSYSLTISS  76
           : ||||||||
Qy     89  SDYSLTISS  97

Query Match                    85.2%;   Score 46;   DB 1;  Length 107;
Best Local Similarity          77.8%;   Pred. No. 4.26e+00;   Indels  0;   Gaps  0;
Matches    7;   Conservative   1;   Mismatches   1;
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RESULT   14
ID   KV6A_MOUSE     STANDARD;      PRT;    107 AA.
AC   P01675;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-VI REGION (XRPC 44).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 79082830.
RA   RAO D.N., RUDIKOFF S., POTTER M.;
RL   BIOCHEMISTRY 17:5555-5559(1978).
DR   PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ.
CC   -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.
KW   IMMUNOGLOBULIN V REGION.
FT   DOMAIN        1     23      FRAMEWORK 1.
FT   DOMAIN       24     33      COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       34     48      FRAMEWORK 2.
FT   DOMAIN       49     55      COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       56     87      FRAMEWORK 3.
FT   DOMAIN       88     96      COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       97    106      FRAMEWORK 4.
FT   DISULFID     23     87      BY SIMILARITY.
FT   NON_TER     107    107
SQ   SEQUENCE    107 AA;   11627 MW;  2EF7479 CRC32;

Db     68  TSYSLTISS  76
           : ||||||||
Qy     89  SDYSLTISS  97

Query Match                    85.2%;   Score 46;   DB 1;  Length 107;
Best Local Similarity          77.8%;   Pred. No. 4.26e+00;   Indels  0;   Gaps  0;
Matches    7;   Conservative   1;   Mismatches   1;
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```
RESULT   15
ID   KV6B_MOUSE     STANDARD;      PRT;    107 AA.
AC   P01676;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-VI REGION (XRPC 24).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 79082830.
RA   RAO D.N., RUDIKOFF S., POTTER M.;
RL   BIOCHEMISTRY 17:5555-5559(1978).
     PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ.
KW   IMMUNOGLOBULIN V REGION.
CC   -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BIND GALACTAN.
FT   DOMAIN        1     23      FRAMEWORK 1.
FT   DOMAIN       24     33      COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       34     48      FRAMEWORK 2.
FT   DOMAIN       49     55      COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       56     87      FRAMEWORK 3.
FT   DOMAIN       88     96      COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       97    106      FRAMEWORK 4.
FT   DISULFID     23     87      BY SIMILARITY.
FT   NON_TER     107    107
SQ   SEQUENCE    107 AA;   11584 MW;  91B2CD6E CRC32;

Db     68  TSYSLTISS  76
           : ||||||||
Qy     89  SDYSLTISS  97

Query Match                    85.2%;   Score 46;   DB 1;  Length 107;
Best Local Similarity          77.8%;   Pred. No. 4.26e+00;   Indels  0;   Gaps  0;
Matches    7;   Conservative   1;   Mismatches   1;

Search completed: Tue Apr 20 14:07:25 1999
Job time : 5 secs.
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MPSRCH (TM)

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

on: Tue Apr 20 14:07:44 1999;   MasPar time 4.19 Seconds
                                          106.989 Million cell updates/sec

Tabular output not generated.

Sequence: 1 SDYSLISS 9
Perfect Score: 54
Description: (89-97) from trans.pep (3 of 3)
Title: >US-08-836-455-1_1

Database: sptrembl6
                1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
                5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
                9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
                13:sp_vertebrate 14:sp_virus

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Searched: 165420 seqs, 49795644 residues

Scoring table: PAM 150
                Gap 11

Statistics: Mean 21.822; Variance 24.944; scale 0.875

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	50	92.6	99	11	P97409	TYPE II COLLAGEN ANTI-	1.61e+00
2	50	92.6	107	11	035538	KAPPA (FRAGMENT).	1.61e+00
3	50	92.6	117	4	090478	IMMUNOGLOBULIN VARIABL	1.61e+00
4	48	88.9	1197	13	058025	ADHESION MOLECULE L1.1	1.61e+00
5	46	85.2	787	1	016077	787AA LONG HYPOTHETICA	4.54e+00
6	45	83.3	93	4	016078	RHEUMATOID FACTOR KAPP	1.25e+01
7	45	83.3	93	4	016078	RF-V KAPPA 1=RHEUMATOI	2.04e+01
8	45	83.3	105	4	099514	LIGHT CHAIN FAB FRAGME	2.04e+01
9	45	83.3	107	4	099953	VASOACTIVE INTESTINAL	2.04e+01
10	45	83.3	113	4	014540	HRV FAB 027-VL (FRAGMEN	2.04e+01
11	45	83.3	113	4	014535	HRV FAB N6-VL (FRAGMEN	2.04e+01
12	45	83.3	115	4	099826	ANTI-HIV-1 GP120 V3 LO	2.04e+01
13	45	83.3	115	4	015986	RHEUMATOID FACTOR D5 L	2.04e+01
14	45	83.3	118	4	043690	ANTI-MPL SCFV (FRAGMEN	2.04e+01
15	45	83.3	239	4	000289	SINGLE-CHAIN FV FRAGME	2.04e+01
16	45	83.3	240	4	000288	SINGLE-CHAIN FV FRAGME	2.04e+01
17	45	83.3	244	4	043689	ANTI-HER3 SCFV (FRAGME	2.04e+01
18	45	83.3	244	5	016768	R07C3.8 PROTEIN.	2.04e+01
19	45	83.3	381	4	060308	RF-V KAPPA 1=RHEUMATOI	2.04e+01
20	44	81.5	925	4	016079	RF-V KAPPA 1-RHEUMATOI	3.31e+01
21	44	81.5	108	4	099818	ANTI-SSDNA ANTIBODY LI	3.31e+01
22	44	81.5	116	4	015982	RHEUMATOID FACTOR C6 L	3.31e+01
23	44	81.5	291	1	055498	291AA LONG HYPOTHETICA	3.31e+01
24	44	81.5	300	1	086635	300AA LONG HYPOTHETICA	3.31e+01
25	43	79.6	127	11	061251	ANTIGEN, B-CELL RECEPT	5.34e+01
26	43	79.6	132	5	021727	COSMID R04E5.	5.34e+01
27	43	79.6	243	11	035140	ANTI-CD30 MOAB KI-4 SC	5.34e+01
28	43	79.6	327	2	050299	HYPOTHETICAL 38.0 KD P	5.34e+01
29	43	79.6	346	2	051194	HYPOTHETICAL 40.3 KD P	5.34e+01
30	43	79.6	359	2	068206	UDP-GALACTOSE:(GLUCOSY	5.34e+01
31	43	79.6	520	2	047163	UDP-GALACTOSE:(GLUCOSY	5.34e+01
32	43	79.6	974	2	008166	(CTR5X).	5.34e+01
33	43	79.6	2971	8	032065	HYPOTHETICAL 341.7 KD	5.34e+01
34	42	77.8	133	11	061551	CC49 FAB PRECURSOR (FR	8.53e+01
35	42	77.8	186	2	025653	SITE-SPECIFIC RECOMBIN	8.53e+01
36	42	77.8	248	11	053818	IMMUNOTOXIN MIK-BETA 1	8.53e+01
37	42	77.8	341	5	062472	Y45F10B.6.	8.53e+01
38	42	77.8	414	14	057752	HYPOTHETICAL 49.5 KD P	8.53e+01
39	42	77.8	470	5	016776	F28F8.2.	8.53e+01
40	42	77.8	618	5	018693	R07C3.3 PROTEIN.	8.53e+01
41	42	77.8	620	2	P77890	RNA POLYMERASE SIGMA F	8.53e+01
42	42	77.8	1232	13	090284	L1-LIKE CELL ADHESION	8.53e+01
43	42	77.8	2335	3	014356	PUTATIVE PHOSPHATIDYLI	8.53e+01
44	42	77.8	6632	5	017362	UNC-89.	8.53e+01
45	42	77.8	6642	5	001761	C. ELEGANS UNC-89 (GB:	8.53e+01

ALIGNMENTS

```
RESULT 1
ID   P97409      PRELIMINARY;   PRT;   99 AA.
AC   P97409;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   TYPE II COLLAGEN ANTI-IDIOTYPIC ANTIBODY KAPPA LIGHT CHAIN VARIABLE
DE   REGION (FRAGMENT).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE; 97257994.
RA   ITO H.O., UEDA T., HASHIMOTO Y., IMOTO T., KOGA T.;
RL   CELL. MOL. LIFE SCI 53:51-60(1997).
DR   EMBL; U69540; G1731669; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER      1      1
FT   NON_TER     99     99
SQ   SEQUENCE   99 AA;  10958 MW;  8B07C16F CRC32;

Qy   90 DYSLISS 97
          |||||||
Db   67 DYSLISS 74

Query Match      92.6%;   Best Local Similarity 100.0%;
Matches    8;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Score 50;  DB 11;  Length 99;
Pred. No. 1.61e+00;


RESULT 2
ID   035538      PRELIMINARY;   PRT;   107 AA.
AC   035538;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   KAPPA (FRAGMENT).
GN   KAPPA.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
```

RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   UDA T., HIFUMI E., ISHIMARU M., MORIHARA F., ITOH T.;
RL   J. FERMENT. BIOENG. 83:333-340(1997).
DR   EMBL; D55701; D1024447; -.
DR   EMBL; D86361; D1024550; -.
DR   PFAM; PF00047; ig.
FT   NON_TER   1   1
FT   NON_TER   107   107
SQ   SEQUENCE   107 AA; 11933 MW; 3BF775AC CRC32;

Query Match   92.6%; Score 50; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.61e+00;
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   70 DYSLTISS 77
              ||||||||
Qy   90 DYSLTISS 97

RESULT 3
ID   O15358
AC   O15358;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   IMMUNOGLOBULIN VARIABLE REGION, KAPPA LIGHT CHAIN (FRAGMENT).
GN   VKLA.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RA   JUUL L., HOGGS L., BARINGTON T.;
RL   SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; Y14865; E1169998; -.
DR   PFAM; PF00047; ig.
FT   NON_TER   117   117
SQ   SEQUENCE   117 AA; 12748 MW; 0340B1EF CRC32;

Query Match   92.6%; Score 50; DB 4; Length 117;
Best Local Similarity 77.8%; Pred. No. 1.61e+00;
Matches   7; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy   91 TDYTLTISS 99
              ::||:|||||
Db   89 SDYSLTISS 97

RESULT 4
ID   Q90478
AC   Q90478;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   ADHESION MOLECULE L1.1 (FRAGMENT)
OS   BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES;
OC   OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96155762.
RA   TONGIORGI E., BERNHARDT R.R., SCHACHNER M.;
RL   J. NEUROSCI. RES. 42:547-561(1995).
DR   EMBL; X89204; G1065714; -.
DR   PFAM; PF00041; fn3.
FT   NON_TER   1   1
SQ   SEQUENCE 1197 AA; 132860 MW; 6D9423C0 CRC32;

Query Match   88.9%; Score 48; DB 13; Length 1197;
Best Local Similarity 66.7%; Pred. No. 4.54e+00;

Matches   6; Conservative   3; Mismatches   0; Indels   0; Gaps   0;

Db   825 SDYTLITA 833
              |||:||:::
Qy   89 SDYSLTISS 97

RESULT 5
ID   O58025
AC   O58025;
DT   01-AUG-1998 (TREMBLREL. 07, CREATED)
DT   01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   787AA LONG HYPOTHETICAL PROTEIN.
GN   PHBM045.
OS   PYROCOCCUS HORIKOSHII.
OC   ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OT3;
RA   KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
RA   YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
RA   SAKAI M., OGURA K., OTSUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
RA   FUNAHASHI T., TANARA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
RA   AOKI K., YOSHIZAWA T., NAKAMURA Y., MASUCHI Y., SHIZUYA H., KIKUCHI H.;
RL   SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB009473; D1027408; -.
SQ   SEQUENCE   787 AA; 86903 MW; B47F09A6 CRC32;

Query Match   85.2%; Score 46; DB 1; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.25e+01;
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   564 SDYSLTI 570
              |||||||
Qy   89 SDYSLTI 95

RESULT 6
ID   Q16077
AC   Q16077;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   RHEUMATOID FACTOR KAPPA CHAIN VJ REGION (FRAGMENT)
RF   V<KAPPA>1.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94033036.
RA   MARTIN T., CROUZIER R., BLAISON G., LEVALLOIS H., PASQUALI J.L.;
RL   AUTOIMMUNITY 15:163-170(1993).
DR   EMBL; S67059; E98153; -.
DR   PFAM; PF00047; ig.
FT   NON_TER   1   1
SQ   SEQUENCE   93 AA; 10082 MW; 3A915983 CRC32;

Query Match   83.3%; Score 45; DB 4; Length 93;
Best Local Similarity 66.7%; Pred. No. 2.04e+01;
Matches   6; Conservative   3; Mismatches   0; Indels   0; Gaps   0;

Qy   89 SDYSLTISS 97
              ::|||:||||
Db   85 TDYTLTISS 93

RESULT 7
ID   Q16078
AC   Q16078;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)

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DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   RF-V KAPPA 1-RHEUMATOID FACTOR V KAPPA REGION (CLONE SLKV7)
DE   (FRAGMENT).
GN   RF-V<KAPPA>-1.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94033036.
RA   MARTIN T., CROZIER R., BLAISON G., LEVALLOIS H., PASQUALI J.L.;
RL   AUTOIMMUNITY 15:163-170(1993).
DR   EMBL; S67060; E98154; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER       1      1
FT   NON_TER      93     93
SQ   SEQUENCE   93 AA;  10178 MW;  6110E33C1 CRC32;

Qy          89 SDYSLTISS 97

Db          54 TDFTLTISS 62
               :|::|||||

Query Match     Best Local Similarity 66.7%;  Score 45;  DB 4;  Length 93;
Matches   6;  Conservative 3;  Pred. No. 2.04e+01;  Mismatches 0;  Indels 0;  Gaps 0;


RESULT 8
ID   Q99514       PRELIMINARY;       PRT;   105 AA.
AC   Q99514;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   LIGHT CHAIN FAB FRAGMENT (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   HORN M.P., VOGEL M., BIAGGI C., MIESCHER S.M., STADLER B.M.;
RL   SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; Y08148; E274854; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER       1      1
FT   NON_TER     105    105
SQ   SEQUENCE  105 AA;  11303 MW;  249B7EC3 CRC32;

Qy          89 SDYSLTISS 97

Db          67 TDFTLTISS 75
               :|::|||||

Query Match     Best Local Similarity 66.7%;  Score 45;  DB 4;  Length 105;
Matches   6;  Conservative 3;  Pred. No. 2.04e+01;  Mismatches 0;  Indels 0;  Gaps 0;


RESULT 9
ID   Q99953       PRELIMINARY;       PRT;   107 AA.
AC   Q99953;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   VASOACTIVE INTESTINAL POLYPEPTIDE HYDROLYZING AUTOANTIBODY LIGHT CHAIN
DE   (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   TYUTYULKOVA S., GAO Q.S., THOMPSON A., RENNARD S., PAUL S.;
RL   BIOCHIM. BIOPHYS. ACTA 1316:217-223(1996).
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DR   EMBL; L43499; G1850134; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE  107 AA;  11468 MW;  3D1FEE15 CRC32;

Qy          89 SDYSLTISS 97

Db          69 TDFTLTISS 77
               :|::|||||

Query Match     Best Local Similarity 66.7%;  Score 45;  DB 4;  Length 107;
Matches   6;  Conservative 3;  Pred. No. 2.04e+01;  Mismatches 0;  Indels 0;  Gaps 0;


RESULT 10
ID   O14540       PRELIMINARY;       PRT;   113 AA.
AC   O14540;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   HRV FAB 027-VL (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PBL;
RA   ITOH K., SUZUKI T.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB006849; D1023047; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER     113    113
SQ   SEQUENCE  113 AA;  12383 MW;  FCEB1F02 CRC32;

Qy          89 SDYSLTISS 97

Db          71 TDFTLTISS 79
               :|::|||||

Query Match     Best Local Similarity 66.7%;  Score 45;  DB 4;  Length 113;
Matches   6;  Conservative 3;  Pred. No. 2.04e+01;  Mismatches 0;  Indels 0;  Gaps 0;


RESULT 11
ID   O14535       PRELIMINARY;       PRT;   113 AA.
AC   O14535;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   HRV FAB N6-VL (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PBL;
RA   ITOH K., SUZUKI T.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB006842; D1023041; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER     113    113
SQ   SEQUENCE  113 AA;  12207 MW;  A546C704 CRC32;

Qy          89 SDYSLTISS 97

Db          71 TDFTLTISS 79
               :|::|||||

Query Match     Best Local Similarity 66.7%;  Score 45;  DB 4;  Length 113;
Matches   6;  Conservative 3;  Pred. No. 2.04e+01;  Mismatches 0;  Indels 0;  Gaps 0;
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```
RESULT 12
ID    Q99826                    PRELIMINARY;      PRT;    115 AA.
AC    Q99826;
DT    01-MAY-1997 (TREMBLREL. 03, CREATED)
DT    01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT    01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE    ANTI-HIV-1 GP120 V3 LOOP ANTIBODY DO142-10 LIGHT CHAIN VARIABLE REGION
DE    (FRAGMENT).
OS    HOMO SAPIENS (HUMAN).
OC    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC    EUTHERIA; PRIMATES.
RN    [1]
RP    SEQUENCE FROM N.A.
RA    DITZEL H.J., PARREN P.W.H.I., BINLEY J.M., SODROSKI J., MOORE J.P.,
RA    BARBAS C.F., BURTON D.R.;
RL    SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR    EMBL; U82962; G1800287; -.
DR    PFAM; PF00047; ig.
NON_TER 1 1
SEQUENCE 115 AA;  12740 MW;  7450103A CRC32;
Qy    89 SDYSLTISS 97

Db    75 TDFTLTISS 83
         :|:||||||
Query Match              83.3%;  Score 45;  DB 4;  Length 115;
Best Local Similarity    66.7%;  Pred. No. 2.04e+01;
Matches    6;  Conservative   3;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT 13
ID    Q15986                    PRELIMINARY;      PRT;    118 AA.
AC    Q15986;
DT    01-NOV-1996 (TREMBLREL. 01, CREATED)
DT    01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT    01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE    RHEUMATOID FACTOR D5 LIGHT CHAIN (FRAGMENT).
GN    V<KAPPA>3.
OS    HOMO SAPIENS (HUMAN).
OC    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC    EUTHERIA; PRIMATES.
RN    [1]
RP    SEQUENCE FROM N.A.
RA    ERMEL R.W., KENNY T.P., CHEN P.P., ROBBINS D.L.;
RL    ARTHRITIS RHEUM. (MUNCH.) 36:380-388(1993).
EMBL; S56199; G298553; -.
PFAM; PF00047; ig.
NON_TER 1 1
NON_TER 118 118
SEQUENCE 118 AA;  12766 MW;  D2815206 CRC32;
Qy    89 SDYSLTISS 97

Db    69 TDFTLTISS 77
         :|:||||||
Query Match              83.3%;  Score 45;  DB 4;  Length 118;
Best Local Similarity    66.7%;  Pred. No. 2.04e+01;
Matches    6;  Conservative   3;  Mismatches   0;  Indels   0;  Gaps   0;

RA    GODDARD A., YUAN J., ZHU Z., CARTER P.;
RL    SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR    EMBL; AF048775; G2911502; -.
NON_TER 1 1
SEQUENCE 239 AA;  25262 MW;  5B9ABF4C CRC32;
Qy    89 SDYSLTISS 97

Db    201 TDFTLTISS 209
         :|:||||||
Query Match              83.3%;  Score 45;  DB 4;  Length 239;
Best Local Similarity    66.7%;  Pred. No. 2.04e+01;
Matches    6;  Conservative   3;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT 15
ID    O00289                    PRELIMINARY;      PRT;    240 AA.
AC    O00289;
DT    01-JUL-1997 (TREMBLREL. 04, CREATED)
DT    01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT    01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE    SINGLE-CHAIN FV FRAGMENT (FRAGMENT).
GN    SCFV.
OS    HOMO SAPIENS (HUMAN).
OC    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC    EUTHERIA; PRIMATES.
RN    [1]
RP    SEQUENCE FROM N.A.
RA    KONTERMANN R.E., WING M.G., WINTER G.;
RL    NAT. BIOTECHNOL. 15:629-631(1997).
DR    EMBL; Y13056; E315281; -.
PFAM; PF00047; ig.
NON_TER 1 1
SEQUENCE 240 AA;  25569 MW;  6472A9C9 CRC32;
Qy    89 SDYSLTISS 97

Db    201 TDFTLTISS 209
         :|:||||||
Query Match              83.3%;  Score 45;  DB 4;  Length 240;
Best Local Similarity    66.7%;  Pred. No. 2.04e+01;
Matches    6;  Conservative   3;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT 14
ID    O43690                    PRELIMINARY;      PRT;    239 AA.
AC    O43690;
DT    01-JUN-1998 (TREMBLREL. 06, CREATED)
DT    01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT    01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE    ANTI-MPL SCFV (FRAGMENT).
OS    HOMO SAPIENS (HUMAN).
OC    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC    EUTHERIA; PRIMATES.
RN    [1]
RP    SEQUENCE FROM N.A.
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Search completed: Tue Apr 20 14:08:04 1999

Job time : 20 secs.

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*********************************************

          M P S R C H  (TM)

*********************************************
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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

         on: Tue Apr 20 13:56:56 1999; MasPar time 2.84 Seconds
                                          28.502 Million cell updates/sec

Title: tabular output not generated.
Description: >US-08-836-455-2
              (31-35) from US08836455.pep (1 of 3)
Perfect Score: 28
Sequence: 1 LSASL 5

Scoring table: PAM 150
                Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: a-geneseq32
           1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
           8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
           14:part14 15:part15 16:part16 17:part17 18:part18
           19:part19 20:part20 21:part21 22:part22 23:part23
           24:part24 25:part25 26:part26 27:part27 28:part28
           29:part29

Statistics: Mean 11.770; Variance 31.125; scale 0.378

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES

Result   %   Query
No.   Score Match Length DB ID   Description   Pred. No.
---- ----- ----- ------ -- ------ -----------   --------
  1   28   100.0   90   16 R80078 Mouse derived light c   1.47e+03
  2   28   100.0   90   16 R80079 Mouse derived light c   1.47e+03
  3   28   100.0 106   15 R81328 Mouse anti-VLA-4 anti   1.47e+03
  4   28   100.0 107   25 W27121 Murine antibody light   1.47e+03
  5   28   100.0 107   5 R27499 WN1 222-5 antibody li   1.47e+03
  6   28   100.0 107   6 R30768 Murine anti-CD3 MAb U   1.47e+03
  7   28   100.0 108   25 W16620 Anti-human FasL antib   1.47e+03
  8   28   100.0 108   18 R93159 Murine monoclonal ant   1.47e+03
  9   28   100.0 108   4 R21286 Murine VL kappa group   1.47e+03
 10   28   100.0 109   25 W18270 Prp 28 light chain va   1.47e+03
 11   28   100.0 126   24 W22409 Alpha-4 integrin mous   1.47e+03
 12   28   100.0 126   15 R81332 Human VLA-4 antibody   1.47e+03
 13   28   100.0 126   15 R81326 Mouse VLA-4 antibody   1.47e+03
 14   28   100.0 126   2 R12237 Mouse MAb 1C11 L chai   1.47e+03
 15   28   100.0 127   20 R99003 MAb VL17E6 light chai   1.47e+03
 16   28   100.0 127   23 W1815   Mouse anti-human chal   1.47e+03
 17   28   100.0 127   6 R28670 Mouse anti-human Fas   1.47e+03
 18   28   100.0 127   8 R39265 Mouse C4G1 Ig light-c   1.47e+03
 19   28   100.0 128   8 R40174 Humanised IL-5 antibo   1.47e+03
 20   28   100.0 128   1 R06252 Variable region of mu   1.47e+03
 21   28   100.0 129   24 W22537 Murine anti-human cla   1.47e+03
 22   28   100.0 129   2 R11057 Feline immunoglobulin   1.47e+03
 23   28   100.0 178   1 R82943 N-terminal of leukaem   1.47e+03
 24   28   100.0 203   2 R33379 Cytokine mIIF.   1.47e+03
 25   28   100.0 203   17 R88201 Murine leukaemia inhi   1.47e+03
 26   28   100.0 214   4 R82945 Leukaemia Inhibitory   1.47e+03
 27   28   100.0 214   6 R30776 H52L6-158 murine anti   1.47e+03
 28   28   100.0 240   15 R85495 ScFv(FWP51).   1.47e+03
 29   28   100.0 284   29 W55375 H. pylori ORF 0ee0107   1.47e+03
 30   28   100.0 284   17 W55369 Intracellular binding   1.47e+03
 31   28   100.0 355   28 W35133 H. pylori cytoplasmic   1.47e+03
 32   28   100.0 391   22 W21016 H. pylori recombinan   1.47e+03
 33   28   100.0 405   3 R14838 H. pipiens recombin   1.47e+03
 34   28   100.0 436   4 R88468 Truncated precursor o   1.47e+03
 35   28   100.0 437   17 R88468 Human two chain facto   1.47e+03
 36   28   100.0 495   8 R22511 Human carbastatin-lik   1.47e+03
 37   28   100.0 495   4 R42949 Envelope protein enco   1.47e+03
 38   28   100.0 523   1 R05701 NtrA gene product.   1.47e+03
 39   28   100.0 591   23 R25072 Mouse apoptosis inhib   1.47e+03
 40   28   100.0 629   5 R25072 H13 gene product.   1.47e+03
 41   28   100.0 647   2 P93971 Human Factor Xa1.   1.47e+03
 42   28   100.0 673   1 R05701 Human carbastatin pol   1.47e+03
 43   28   100.0 682   17 R87154 Alternatively spliced   1.47e+03
 44   28   100.0 866   28 W31630 Aspergillus oryzae Ar   1.47e+03
 45   28   100.0 1342   16 R88453 erbB-3 polypeptide.   1.47e+03
```

                                ALIGNMENTS

```
RESULT 1

ID   R80078 standard; Protein; 90 AA.
AC   R80078;
DT   22-MAY-1996 (first entry)
DE   Mouse derived light chain RT3 phage antibody pattern A.
KW   Light chain; RT3; murine; catalytic antibody; bacteriophage;
OS   Mus musculus.
FH   Key              Location/Qualifiers
FT   region           1..15
FT                    /note= "framework region 1"
FT   region           16..26
FT                    /note= "complementarity determining region 1"
FT   region           27..40
FT                    /note= "framework region 2"
FT   region           41..47
FT                    /note= "complementarity determining region 2"
FT   region           48..78
FT                    /note= "framework region 3"
FT   region           79..88
FT                    /note= "complementarity determining region 3"
FT   region           89..90
FT                    /note= "framework region 4
FT                    N-terminal fragment"
PN   WO9527045-A1.
PD   12-OCT-1995.
PF   30-MAR-1994; U03420.
PR   30-MAR-1994; WO-U03420.
PA   (IGEN-) IGEN INC.
PI   Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI   Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;
DR   WPI; 95-358624/46.
DR   N-PSDB; T04625.
PT   Production of catalytic antibodies displayed on phage - by
PT   generating a gene library of antibody-derived domains and expressing
PT   it in phage vectors
PS   Disclosure; Fig 9; 133pp; English.
PT   T04625 encodes R80078 mouse derived light chain RT3 phage antibody.
CC   The DNA was used in the prepn. of catalytic antibody.(CA) producing
CC   bacteriophage. The CAs can be used to activate/deactivate a
CC   biological function in an animal by enhancing the rate of cleavage,
CC   or formation of a specific bond within a mol. in vivo.
```

SQ   Sequence   90 AA;

Query Match   100.0%;   Score 28;   DB 16;   Length 90;
Best Local Similarity 100.0%; Pred. No. 1.47e+03;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   3 1sasl 7
           |||||
Qy   31 LSASL 35

RESULT 2
ID   R80079 standard; Protein; 90 AA.
AC   R80079;
DT   22-MAY-1996 (first entry)
DE   Mouse derived light chain RT3 phage antibody pattern C.
KW   Light chain; RT3; murine; catalytic antibody; bacteriophage;
     pattern C.
OS   Mus musculus.
FT   Key   Location/Qualifiers
FT   region   1..15
FT   /note= "framework region 1"
FT   region   16..26
FT   /note= "complementarity determining region 1"
FT   region   27..40
FT   /note= "framework region 2"
FT   region   41..47
FT   /note= "complementarity determining region 2"
FT   region   48..78
FT   /note= "complementarity determining region 2"
FT   region   79..88
FT   /note= "framework region 3"
FT   region   89..90
FT   /note= "complementarity determining region 3"
FT   region
FT   /note= "framework region 4"
FT   /note= N-terminal fragment"

PN   WO9527045-A1.
PD   12-OCT-1995.
PF   30-MAR-1994; U03420.
PR   30-MAR-1994; WO-U03420.
PA   (IGEN-) IGEN INC.
PI   Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI   Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;
DR   WPI; 95-358624/46.
DR   N-PSDB; T04626.
PT   Production of catalytic antibodies displayed on phage - by
PT   generating a gene library of antibody-derived domains and expressing
PT   it in phage vectors
PT   Disclosure; Fig 9; 133pp; English.
CC   T04626 encodes R80079 mouse derived light chain RT3 phage antibody.
CC   The DNA was used in the prepn. of catalytic antibody (CA) producing
CC   bacteriophage. The CAs can be used to activate/deactivate a
CC   biological function in an animal by enhancing the rate of cleavage,
CC   or formation of a specific bond within a mol. In vivo.
SQ   Sequence 90 AA;

Query Match   100.0%;   Score 28;   DB 16;   Length 90;
Best Local Similarity 100.0%; Pred. No. 1.47e+03;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   3 1sasl 7
           |||||
Qy   31 LSASL 35

RESULT 3
ID   R81328 standard; Protein; 106 AA.
AC   R81328;
DT   02-APR-1996 (first entry)
DE   Mouse anti-VLA-4 antibody 21.6 light chain variable region.
KW   Humanized antibody; antibody engineering; leukocyte adhesion molecule; VLA-4; therapeutic;
OS   Mus musculus.
FH   Key   Location/Qualifiers
FT   region   1..23
FT   /label= FR1
FT   /note= "mouse light chain variable framework
FT   region 1"
FT   region   24..34
FT   /label= CDR1
FT   /note= "mouse light chain variable complementarity
FT   determining region 1"
FT   region   35..49
FT   /label= FR2
FT   /note= "mouse light chain variable framework
FT   region 2"
FT   region   50..56
FT   /label= CDR2
FT   /note= "mouse light chain variable complementarity
FT   determining region 2"
FT   region   57..88
FT   /label= FR3
FT   /note= "mouse light chain variable framework
FT   region 3"
FT   region   89..96
FT   /label= CDR3
FT   /note= "mouse light chain variable complementarity
FT   determining region 3"
FT   region   97..106
FT   /label= FR4
FT   /note= "mouse light chain variable framework
FT   region 4"

PN   WO9519790-A1.
PD   27-JUL-1995.
PF   25-JAN-1995; U01219.
PR   25-JAN-1994; US-1186269.
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
PI   Bendig MM, Jones TS, Leger OJ, Saldanha J;
DR   WPI; 95-269276/35.
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
PS   Disclosure; Page 66; 105pp; English.
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain in the construction of a humanized
CC   antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See Q99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light chain.
CC   Plasmids encoding the chimeric antibodies are transfected into COS cells.
CC   The humanized antibodies can be used to inhibit adhesion of a leukocyte
CC   to an endothelial cell and to treat inflammatory diseases such as
CC   multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
SQ   Sequence 106 AA;

Query Match   100.0%;   Score 28;   DB 15;   Length 106;
Best Local Similarity 100.0%; Pred. No. 1.47e+03;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   11 1sasl 15
           |||||
Qy   31 LSASL 35

RESULT 4
ID   W27121 standard; Protein; 107 AA.
AC   W27121;
DT   04-JAN-1998 (first entry)
DE   Murine antibody light chain variable region consensus.

```
KW   Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
KW   human milk fat globule; HMFG; tumour; breast cancer; vaccine.
OS   Mus musculus.
FH   Key              Location/Qualifiers
FT   Region           24..34
FT                    /label= CDR1
FT   Region           50..56
FT                    /note= "complementarity determining region 1"
FT   Region           50..56
FT                    /label= CDR2
FT                    /note= "complementarity determining region 2"
FT   Region           88..96
FT                    /label= CDR3
FT                    /note= "complementarity determining region 3"
          (KENT ) UNIV KENTUCKY.
PN   WO9722699-A2.
PD   26-JUN-1997.
PF   19-DEC-1996; U20757.
PR   13-DEC-1996; US-575762.
PR   20-DEC-1995; US-575762.
PR   26-JAN-1996; US-591965.
WPI: 97-341690/31
Chatterjee M, Chatterjee SK, Foon KA;
PT   Monoclonal anti-idiotype antibody 11D10 - elicits immune response
PT   against human milk fat globule disease associated tumours,
PT   especially breast cancer
PS   Example 2; Fig 26C; 130pp; English.
CC   This polypeptide sequence comprises a consensus sequence of murine
CC   light chain variable regions (VL) selected on the basis of identity
CC   to the VL region (see W27119) of monoclonal anti-idiotype antibody
CC   11D10. The sequences were obtained from a GenBank database
CC   search. A VH consensus (W27122) was also produced. 11D10 has at
CC   least 18 departures from the consensus sequences (7 in the light
CC   chain and 11 in the heavy chain). 8 occur within CDRS and 10
CC   outside CDRs. 11D10 polypeptides and polynucleotides can be
CC   used in vaccines and pharmaceutical compositions for the treatment
CC   of human milk fat globule-associated diseases such as breast
CC   cancer.
SQ   Sequence 107 AA;

Db   11 lsasl 15
        |||||
Qy   31 LSASL 35

Query Match          100.0%;        Score 28;  DB 25;  Length 107;
Best Local Similarity 100.0%;        Pred. No. 1.47e+03;
Matches              5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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UlIr  5
AC   R27499 standard; Protein; 107 AA.
     R27499;
DT   10-MAR-1993 (first entry)
DE   WN1 222-5 antibody Light chain Variable domain.
KW   Monoclonal antibody; MAb; epitope; core region; LPS;
KW   lipopolysaccharide; endotoxaemia; WN1 222-5; WN1 58-9;
KW   light; heavy; Gram-negative bacteria.
OS   Mus musculus.
FH   Key              Location/Qualifiers
FT   region           1..23
FT                    /label= 1FR1
FT   region           24..34
FT                    /label= 1CDR1
FT   region           35..49
FT                    /label= 1FR2
FT   region           50..56
FT                    /label= 1CDR2
FT   region           57..88
FT                    /label= 1FR3
FT   region           89..97
FT                    /label= 1CDR3
FT   region           98..107
FT                    /label= 1FR4

Db   11 lsasl 15
        |||||
Qy   31 LSASL 35

Query Match          100.0%;        Score 28;  DB 5;  Length 107;
Best Local Similarity 100.0%;        Pred. No. 1.47e+03;
Matches              5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
PD   01-OCT-1992.
PF   22-FEB-1992; E00380.
PR   13-MAR-1991; GB-005292.
PA   (SANO ) SANDOZ LTD.
PA   (SANO ) SANDOZ PATENT GMBH.
PI   Barclay GR, Di Padova F, Gram H, Poxton IR;
DR   N-PSDB; Q29150.
DR   WPI; 92-349209/42.
PT   Monoclonal antibodies against LPS core epitope(s) of
PT   Gram-negative bacteria - for diagnosing, preventing and treating
PT   Gram-negative bacterial infections
PS   Claim 23; Page 56 + 43; 82pp; English.
CC   Monoclonal antibodies which recognise an epitope in the core region
CC   of the bacterial lipopolysaccharide (LPS) mol. and which are cross-
CC   protective against endotoxaemia caused by at least two different
CC   Gram-negative bacterial strains having different core structures,
CC   pref. comprise the heavy chain variable domain having the sequence
CC   of R27497 (WN1 222-5) or R27498 (WN1 58-9) and the light chain
CC   variable domain having the sequence of R27499 (WN1 222-5)
CC   or R27500 (WN1 58-9).
SQ   Sequence 107 AA;

Db   11 lsasl 15
        |||||
Qy   31 LSASL 35

Query Match          100.0%;        Score 28;  DB 6;  Length 107;
Best Local Similarity 100.0%;        Pred. No. 1.47e+03;
Matches              5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 6
ID   R30768 standard; protein; 107 AA.
AC   R30768;
DT   12-MAY-1993 (first entry)
DE   Murine anti-CD3 MAb UCHT1 light chain variable domain.
KW   Humanisation; rapid; monoclonal antibody; muxCD3.
OS   Mus musculus.
PN   WO9222653-A.
PD   23-DEC-1992.
PF   15-JUN-1992; U05126.
PR   14-JUN-1991; US-715272.
PA   (GETH ) GENENTECH INC.
PI   Carter PJ, Presta LG;
DR   WPI; 93-018139/02.
PT   Humanisation of antibodies - by molecular modelling of the variable
PT   domains and alteration by gene conversion mutagenesis
PS   Disclosure; Fig 5; 126pp; English.
CC   The sequence is that of the light chain variable domain of murine
CC   anti-CD3 monoclonal antibody UCHT1 (muxCD3, Shalaby 1992).
SQ   Sequence 107 AA;
```

```
RESULT 7
ID   W16620 standard; Protein; 108 AA.
AC   W16620;
DT   14-JAN-1998 (first entry)
DE   Anti-human FasL antibody (NOK1) light chain variable region.
KW   Light chain; variable region; mouse; murine; human; Fas;
KW   FasL; monoclonal antibody; MAb; hybridoma; treatment; hepatitis;
KW   hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis;
KW   liver cell; glutamate oxaloacetate; pyruvate transaminase.
OS   Mus sp.
PN   WO9715326-A1.
PD   01-MAY-1997.
```

PF   24-OCT-1996; J03089.
PR   27-OCT-1995; JP-303491.
PA   (SUME) SUMITOMO ELECTRIC IND CO.
PI   Kayagaki N, Nakata M, Okumura K, Seino K, Yagita H;
DR   WPI; 97-258767/23.
DR   N-PSDB; T66710.
PT   Anti-human Fas Ligand antibody to treat hepatitis - controls
PT   apoptosis in liver cells and improves liver function
PS   Claim 6; Pages 30-31; 51pp; Japanese.
CC   The present sequence is the light chain variable region of the
CC   murine anti-human Fas ligand (FasL) monoclonal antibody (MAb) NOK1,
CC   which is expressed by the hybridoma NOK1 (FERM BP-5044). The Mab
CC   can be used in the preparation of a composition for the effective
CC   oral or parenteral treatment of hepatitis, including hepatitis
CC   caused by hepatitis B or C virus. The composition controls apoptosis
CC   in liver cells caused by the binding of FasL to Fas expressing liver
CC   cells, and improves liver function by improving blood glutamate
CC   oxaloacetate and pyruvate transaminase levels. The composition is
CC   given in a dosage of 0.0001-1000, preferably 0.01-600 mg/day.
CC   Spleen cells from mice immunised with FasL expressing COS cells
CC   were fused with mouse myeloma cells to produce hybridomas. The
CC   hybridomas were screened for anti-FasL activity, and the active
CC   clones NOK1-5 isolated.
SQ   Sequence 108 AA;

Query Match   100.0%; Score 28; DB 25; Length 108;
Best Local Similarity   100.0%; Pred. No. 1.47e+03;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   31 LSASL 35
              |||||
Db   11 lsasl 15

RESULT 8

ID   R93159 standard; Protein; 108 AA.
AC   R93159;
DT   24-OCT-1996 (first entry)
DE   Murine monoclonal antibody K20 kappa chain variable region.
KW   Antibody; light chain; kappa; variable region; K20; integrin; CD29;
KW   beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
KW   T cell activation; complementarity determining region; CDR.
OS   Mus musculus.
FH   Key   Location/Qualifiers
FH
FT   region   1..23
FT   /label= FR1
FT   /note= "framework region"
FT   region   24..34
FT   /label= CDR1
FT   /note= "complementarity determining region"
FT   region   35..49
FT   /label= FR2
FT   /note= "framework region"
FT   region   50..56
FT   /label= CDR2
FT   /note= "complementarity determining region"
FT   region   57..88
FT   /label= FR3
FT   /note= "framework region"
FT   region   89..94
FT   /label= CDR3
FT   /note= "complementarity determining region"
FT   region   95..108
FT   /label= J_kappa1
PN   FR2724393-A1.
PD   15-MAR-1996.
PF   12-SEP-1994; FR-010858.
PR   12-SEP-1994; 010858.
PA   (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (PROT-) PROTEINE PERFORMANCE SA.
PI   Bernard A, Cervoni MF, Lefranc MP, Margaritte C;
PI   Poul MA;
DR   WPI; 96-162083/17.
DR   N-PSDB; T26849.
PT   Humanisation of non-human immunoglobulin variable regions - for
PT   prodn. of humanised antibodies, esp. K20, e.g. as an
PT   immunosuppressant
PS   Example 1; Fig 2A; 39pp; French.
CC   The present sequence is that of the variable region of the kappa
CC   light chain from murine monoclonal antibody K20. The antibody
CC   recognises the beta 1 subunit (CD29) of integrins and inhibits
CC   activation and proliferation of peripheral T cells induced by
CC   anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target
CC   for humanisation; the humanised version may be useful as an
CC   immunosuppressant. In the humanisation process, the complementarity
CC   determining regions (CDRs) of a human antibody with framework
CC   regions 70-95% homologous to those of K20 were replaced by the K20
CC   CDRs.
SQ   Sequence 108 AA;

Query Match   100.0%; Score 28; DB 18; Length 108;
Best Local Similarity   100.0%; Pred. No. 1.47e+03;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   31 LSASL 35
              |||||
Db   11 lsasl 15

RESULT 9

ID   R21286 standard; Protein; 108 AA.
AC   R21286;
DT   21-MAY-1992 (first entry)
DE   Murine VL kappa group V chain "a", specific for phOx.
KW   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW   plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW   specific binding pairs; replicable genetic display package.
OS   Synthetic.
FH   Key   Location/Qualifiers
FH
FT   binding_site   24..34
FT   /label= CDR1
FT   binding_site   50..56
FT   /label= CDR2
FT   binding_site   89..96
FT   /label= CDR3
FT   /note= D-x-G-x-x motif "
PN   WO9201047-A.
PD   23-JAN-1992.
PF   10-JUL-1991; G01134.
PR   10-JUL-1990; GB-015198.
PR   19-OCT-1990; GB-022845.
PR   12-NOV-1990; GB-024503.
PR   06-MAR-1991; GB-004744.
PR   15-MAY-1991; GB-010549.
PA   (MEDI-) MED RES COUNCIL.
PA   (CAMB-) CAMBRIDGE ANTIBODY.
PI   McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI   Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI   Winter GP, Bonnert TP;
DR   WPI; 92-056862/07.
PT   Producing members of specific binding pairs - by expression in
PT   recombinant host cells with a secreting replicable genetic
PT   display package.
PS   Example 21; Fig 24; 209pp; English.
CC   Example 21; Fig 24. 209pp; English.
CC   The VK sequence is one of seven (R21286-92) found to be expressed
CC   from a single chain Fv library from an immunised mouse. The libra-
CC   ry produces a diverse repertoire of antibody fragments specific for
CC   2-phenyl-5-oxazolone (phOx). It was prepd. using cDNA generated
CC   from mRNA from mice immunised with phOx coupled to chicken serum
CC   albumin. The VH and VL kappa sequences were separately amplified
CC   by PCR (see Q23474-84) and ligated into fdCAT2 (see Q23463) for ex-
CC   pression on the phage surface as fusions with gene III. The result-
CC   ing library of clones was diverse. Twenty three hapten binding
CC   clones were sequenced revealing eight different VH genes (A-H) (see
CC   R21264-71) in a variety of pairings with the seven different Vk
CC   genes (a-g). Of the twenty three clones sequenced, three were of

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CC  type "a", and were "ox-like" genes. (See Berek et al, Nature 316
CC  412-418, 1985). They contain the DXGXX motif in CDR3, the central
CC  Gly of which is needed to create a cavity for phox. Most of the
CC  clones were Vk-d combinations. The Kd of VH-B/Vk-d for phox-GABA
CC  was 10 nM. Only two other combinations (of eleven tested) were
CC  found to have higher values. This suggests that phage bearing scFv
CC  fragments having weak affinities can be selected with antigen, pro-
CC  bably due to the avidity of the multiple antibody heads on the
CC  phage.
CC  See also R21260-307, 309-311; R22450, 565-581.
SQ  Sequence  108 AA;

Db  11 lsasl 15
          |||||
Qy  31 LSASL 35

Query Match     100.0%;   Score 28;   DB 4;   Length 108;
Best Local Similarity 100.0%;          Pred. No. 1.47e+03;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 10
ID   W18270 standard; peptide; 109 AA.
AC   W18270;
DT   09-JAN-1998  (first entry)
DE   PrP 28 light chain variable region.
KW   Prion protein; PrP; heavy chain variable region; antibody; scrapie;
KW   light chain variable region; PrP-Sc; pathogen; fatal familial insomnia;
KW   central nervous system spongiform encephalopathy; human; therapy;
KW   transmissible neurodegenerative disease; Creutzfeldt-Jakob Disease;
KW   bovine spongiform encephalopathy; feline spongiform encephalopathy;
KW   Serstmann-Strassler-Scheinker Disease.
OS   Mus musculus.
FH   Key              Location/Qualifiers
FT   Region           1..23
FT                    /note= "framework region 1"
FT   Region           24..34
FT                    /note= "complementarity determining region 1"
FT   Region           35..49
FT                    /note= "framework region 2"
FT   Region           50..56
FT                    /note= "complementarity determining region 2"
FT   Region           57..88
FT                    /note= "framework region 3"
FT   Region           89..97
FT                    /note= "complementarity determining region 3"
FT   Region           98..109
FT                    /note= "framework region 4"
FD   WO9710505-A1.
PD   20-MAR-1997.
PF   13-SEP-1996;  U14840.
PR   14-SEP-1995;  US-528104.
PA   (REGC ) UNIV CALIFORNIA.
PI   Burton DR, Prusiner SB, Williamson RA;
DR   WPI;  97-202357/18.
PT   Example 9; Fig 6; 99pp; English.
PT   New antibodies to the scrapie isoform of prion protein - used for
PT   detection of infectious prion proteins or for treating disease such
PT   as BSE, CJD or scrapie
PT   W18266-W18285 represent portions of the antibodies of the invention. The
PT   antibodies of the invention are able to bind the scrapie isoform of prion
PT   protein PrP-Sc in situ. Prions are infectious pathogens that cause
PT   central nervous system spongiform encephalopathies in humans and animals.
PT   The scrapie isoform of the prion protein (PrP-Sc) is necessary for both
CC   the transmission and pathogenesis of the transmissible neurodegenerative
CC   diseases of animals and humans. The antibodies can be used in a method of
CC   the invention for detecting human PrP-Sc in a source. The antibodies
CC   specifically bind to prion proteins associated with disease and do not
CC   bind to denatured PrP proteins not associated with disease. They can bind
CC   to prion proteins of a specific species of mammals. The antibodies can also have
CC   the ability to neutralise infectious prions. The antibodies can be used
CC   for screening for the presence of prions in products such as
CC   pharmaceuticals, food or cosmetics. They can also be used for prion
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CC   neutralisation to purify products, for extraction of prion proteins or
CC   for therapy, for diseases such as bovine spongiform encephalopathy,
CC   Creutzfeldt-Jakob Disease, fatal familial insomnia or
CC   Serstmann-Strassler-Scheinker Disease, scrapie or feline spongiform
CC   encephalopathies.
SQ   Sequence  109 AA;

Db  11 lsasl 15
          |||||
Qy  31 LSASL 35

Query Match     100.0%;   Score 28;   DB 25;   Length 109;
Best Local Similarity 100.0%;          Pred. No. 1.47e+03;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

RESULT 11
ID   W22409 standard; Protein; 126 AA.
AC   W22409;
DT   08-DEC-1997  (first entry)
DE   Alpha-4 integrin mouse MAb 21.6 VL region.
KW   Alpha-4 integrin mouse MAb 21.6; monoclonal antibody 21.6;
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
OS   Mus musculus.
FH   Key              Location/Qualifiers
FT   peptide          1..20
FT                    /label= Leader
FT   peptide          21..43
FT                    /label= FR1
FT                    /note= "framework region 1"
FT   region           44..54
FT                    /label= CDR1
FT                    /note= "complementarity determining region 1"
FT   region           55..69
FT                    /label= FR2
FT                    /note= "framework region 2"
FT   region           70..76
FT                    /label= CDR2
FT                    /note= "complementarity determining region 2"
FT   region           77..108
FT                    /label= FR3
FT                    /note= "framework region 3"
FT   region           109..116
FT                    /label= CDR3
FT                    /note= "complementarity determining region 3"
FT   region           117..126
FT                    /label= FR4
FT                    /note= "framework region 4"
FD   WO9718838-A1.
PD   29-MAY-1997.
PF   21-NOV-1996;  U18807.
PR   21-NOV-1995;  US-561521.
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
DR   WPI;  97-227879/27.
DR   N-PSDB;  T74759.
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
PS   Claim 18; Page 68; 107pp; English.
PT   This polypeptide comprises the light chain variable region (VL) of
PT   mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
PT   complementarity determining regions (CDRs) of the 21.6 VL can be
PT   incorporated into a human REI framework to produce a claimed
PT   humanised 21.6 VL (see W22412) and a claimed humanised 21.6
CC   antibody that is used in the manufacture of a medicament for
CC   treating a disease selected from asthma, atherosclerosis, AIDS,
CC   dementia, diabetes, transplant rejection, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
```

RESULT 12

Query Match

Best Local Similarity 100.0%;   Score 28; DB 24; Length 126;
Matches 5; Conservative 0; Pred. No. 1.47e+03; Mismatches 0; Indels 0; Gaps 0;

Db 31 lsasl 35
        |||||
Qy 31 LSASL 35

R81332 standard; Protein; 126 AA.
R81332;
23-MAR-1996 (first entry)
Human VLA-4 reshaped antibody 21.6 light chain variable region.
Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
antibody engineering.
Homo sapiens.

Key	Location/Qualifiers
peptide	1..20
	/note= "signal peptide"
region	21..43
	/note= "framework region 1"
region	44..54
	/note= "complementarity determining region 1"
region	55..69
	/note= "framework region 2"
region	70..76
	/note= "complementarity determining region 2"
region	77..108
	/note= "framework region 3"
region	109..116
	/note= "complementarity determining region 3"
region	117..126
	/note= "framework region 4"

WO9519790-A1.
27-JUL-1995.
25-JAN-1995; U01219.
25-JAN-1994; US-186269.
(ATHE-) ATHENA NEUROSCIENCES INC.
Bendig MM, Jones TS, Leger OJ, Saldanha J;
WPI; 95-269276/35.
N-PSDB; Q99893.
Disclosure; Fig 10; 105pp; English.
New humanised antibodies against VLA-4 - used for inhibiting
leukocyte adhesion to endothelial cells, partic. for treating
inflammatory disease.
The sequence represents the human reshaped antibody 21.6 light
chain variable region against leukocyte adhesion molecule VLA-4.
Cloned cDNA sequences of mouse 21.6 VL (Q99889) and VH (Q99892)
regions are linked to human constant regions in the construction
of a humanized antibody against VLA-4. The 5' and 3' ends of the
mouse cDNAs are modified using PCR primers (See Q99895-98) and
then subcloned into mammalian cell expression vectors containing
human kappa or gamma-1 constant regions. In the humanized light
chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR
framework are replaced by the amino acid present in the equivalent
position of the mouse 21.6 Ig L chain. Plasmids encoding the
chimeric antibodies are transfected into COS cells. The humanized
antibodies can be used to inhibit adhesion of a leukocyte to an
endothelial cell and to treat inflammatory diseases such as
multiple sclerosis. They can also be used in the treatment of
stroke, cerebral traumas, meningitis or encephalitis. The
antibodies can also be used for detecting VLA-4, for affinity
purification or for generating anti-idiotype antibodies.
Sequence 126 AA;

RESULT 13

Query Match

Best Local Similarity 100.0%;   Score 28; DB 15; Length 126;
Matches 5; Conservative 0; Pred. No. 1.47e+03; Mismatches 0; Indels 0; Gaps 0;

Db 31 lsasl 35
        |||||
Qy 31 LSASL 35

R81326 standard; Protein; 126 AA.
R81326;
23-MAR-1996 (first entry)
Mouse VLA-4 antibody 21.6 light chain variable region.
Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
antibody engineering.
Mus musculus.

Key	Location/Qualifiers
peptide	1..20
	/note= "signal peptide"
region	21..43
	/note= "framework region 1"
region	44..54
	/note= "complementarity determining region 1"
region	55..69
	/note= "framework region 2"
region	70..76
	/note= "complementarity determining region 2"
region	77..108
	/note= "framework region 3"
region	109..116
	/note= "complementarity determining region 3"
region	117..126
	/note= "framework region 4"

WO9519790-A1.
27-JUL-1995.
25-JAN-1995; U01219.
25-JAN-1994; US-186269.
(ATHE-) ATHENA NEUROSCIENCES INC.
Bendig MM, Jones TS, Leger OJ, Saldanha J;
WPI; 95-269276/35.
N-PSDB; Q99889.
Disclosure; Fig 1; 105pp; English.
New humanised antibodies against VLA-4 - used for inhibiting
leukocyte adhesion to endothelial cells, partic. for treating
inflammatory disease.
The sequence represents the mouse antibody 21.6 light chain variable
region directed against leukocyte adhesion molecule VLA-4. Cloned
cDNA sequences of mouse 21.6 VL and VH (see Q99892) regions are
linked to human constant regions in the construction of a humanized
antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
modified using PCR primers (See Q99895-98) and then subcloned into
mammalian cell expression vectors containing human kappa or gamma-1
constant regions. In the humanized light chain, amino acids L45,
L49, L58 and L69 in the human kappa LC VR framework are replaced
by the amino acid present in the equivalent position of the mouse
21.6 Ig L chain. Plasmids encoding the chimeric antibodies are
transfected into COS cells. The humanized antibodies can be used
to inhibit adhesion of a leukocyte to an endothelial cell and
to treat inflammatory diseases such as multiple sclerosis. They
can also be used in the treatment of stroke, cerebral traumas,
meningitis or encephalitis. The antibodies can also be used for
detecting VLA-4, for affinity purification or for generating
anti-idiotype antibodies.
Sequence 126 AA;

Query Match

Best Local Similarity 100.0%;   Score 28; DB 15; Length 126;
Matches 5; Conservative 0; Pred. No. 1.47e+03; Mismatches 0; Indels 0; Gaps 0;

Db 31 lsasl 35
        |||||

```
Qy            31 LSASL 35

RESULT  14
ID   R12237 standard; Protein; 126 AA.
AC   R12237;
DT   19-AUG-1991 (first entry)
DE   Mouse MAb 1C11 L chain V region.
KW   HIV-1; chimera.
OS   Mus sp.
PN   WO9107494-A.
PD   30-MAY-1991.
PF   13-NOV-1990;
PR   13-NOV-1989; US-433703.
PA   (XOMA-) Xoma Corp.
PI   Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
DR   WPI; 91-178106/24.
DR   N-PSDB; Q12017.
PT   New chimeric mouse human antibodies - used in treatment, diagnosis
PT   and prophylaxis of HIV infections.
CC   The mouse VL gene product may be used to produce chimeric mouse-
CC   human Abs against HIV-1 comprising human Ig constant regions and
CC   murine variable regions. These novel sequence are useful in
CC   treatment, diagnosis and prophylaxis of HIV infections, and may be
CC   produced by a bacterial, yeast or mammalian expression system.
SQ   Sequence 126 AA;

Query Match          100.0%;   Score 28;  DB 2;  Length 126;
Best Local Similarity 100.0%;  Pred. No. 1.47e+03;
Matches    5;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db        31 lsasl 35
             |||||
Qy        31 LSASL 35

RESULT  15
ID   R99003 standard; Protein; 127 AA.
AC   R99003;
DT   10-JAN-1997 (first entry)
DE   MAb VL17E6 light chain (specific for human alphav integrins).
KW   Monoclonal antibody; MAb; integrin; cell-matrix interaction;
KW   tumour; melanoma; glioma; carcinoma; cytokine; interleukin-2; IL-2;
KW   imaging; detection; radiolabel.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   region          21..43
FT                   /label= Framework region 1
FT   binding_site    44..54
FT                   /label= CDR1
FT   region          55..69
FT                   /label= Framework region 2
FT   binding_site    70..76
FT                   /label= CDR2
FT   region          77..108
FT                   /label= Framework region 3
FT   binding_site    109..117
FT                   /label= CDR3
FT   region          118..127
FT                   /label= Framework region 4
PN   EP-719859-A1.
PD   03-JUL-1996.
PF   06-DEC-1995; 119233.
PR   20-DEC-1994; EP-120165.
PA   (MERE ) MERCK PATENT GMBH.
PI   Adan J, Goodman S, Hahn D, Mitjans F, Piulats J;
PI   Rosell E;
DR   WPI; 96-302345/31.
DR   N-PSDB; T35050.
PT   New human integrin v chain-specific monoclonal antibody - and
PT   related DNA and hybridomas, for treatment and diagnostic imaging of
PT   tumours, esp melanoma.

PS   Claim 8; Figure 17a; 54pp; English.
CC   A monoclonal antibody which reacts only with the alphav chain of
CC   human alphaV integrins; which blocks attachment of alphaV integrin
CC   bearing cells to integrin substrate; which reverses established cell
CC   matrix interactions caused by alphaV integrin; which blocks tumour
CC   development and which has no cytotoxic activity, may be used to
CC   treat tumours, especially melanoma (but also glioma, carcinoma)
CC   optionally coupled to a cytokine such as interleukin-2. The
CC   monoclonal antibody may also be used for diagnostic imaging of
CC   tumours and assessment of tumour growth when conjugated to a
CC   radiolabel or a radio opaque-agent.
SQ   Sequence 127 AA;

Query Match          100.0%;   Score 28;  DB 20;  Length 127;
Best Local Similarity 100.0%;  Pred. No. 1.47e+03;
Matches    5;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db        31 lsasl 35
             |||||
Qy        31 LSASL 35

Search completed: Tue Apr 20 13:57:14 1999
Job time : 18 secs.
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MPSRCH (TM)

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Distribution rights by Oxford Molecular Ltd
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```

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

n on: Tue Apr 20 13:56:19 1999; MasPar time 3.21 Seconds
                 58.270 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-836-455-2
                   (31-35) from US08836455.pep (1 of 3)
Perfect Score: 28
Sequence: 1 LSASL 5

Scoring table: PAM 150
                   Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0%
                   Listing first 45 summaries

Database: pir58
                   1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 17.008; Variance 14.078; scale 1.208

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	28	100.0	45	2	S28565	hypothetical protein	6.56e+02
2	28	100.0	93	2	S38564	Ig kappa chain V regi	6.56e+02
3	28	100.0	102	2	S50030	hypothetical protein	6.56e+02
4	28	100.0	106	2	C33936	Ig kappa chain V regi	6.56e+02
5	28	100.0	106	2	PL0259	Ig kappa chain V regi	6.56e+02
6	28	100.0	106	2	PL0260	Ig kappa chain V regi	6.56e+02
7	28	100.0	108	4	B47271	nitrophenyl phosphona	6.56e+02
8	28	100.0	108	2	C26405	Ig kappa chain V regi	6.56e+02
9	28	100.0	108	2	B26405	Ig kappa chain V regi	6.56e+02
10	28	100.0	109	1	KVMS09	Ig kappa chain V regi	6.56e+02
11	28	100.0	109	1	KVMS82	Ig kappa chain V regi	6.56e+02
12	28	100.0	124	2	S03521	Ig kappa chain precur	6.56e+02
13	28	100.0	130	1	KVMSM4	Ig kappa chain precur	6.56e+02
14	28	100.0	138	2	B59465	transcription regulat	6.56e+02
15	28	100.0	165	2	JE0065	retroviral proteinase	6.56e+02
16	28	100.0	177	2	F70508	probable transmembran	6.56e+02
17	28	100.0	182	2	C71214	hypothetical protein	6.56e+02
18	28	100.0	230	2	S33161	Ig kappa chain - shee	6.56e+02
19	28	100.0	245	2	D71554	probable adenylate cy	6.56e+02
20	28	100.0	268	2	A70417	hypothetical protein	6.56e+02
21	28	100.0	280	2	H71320	hypothetical protein	6.56e+02
22	28	100.0	303	2	B47089	probable AraC-type re	6.56e+02
23	28	100.0	304	2	E45277	probable transcriptio	6.56e+02
24	28	100.0	307	2	S67662	hypothetical protein	6.56e+02
25	28	100.0	317	2	S63358	hypothetical protein	6.56e+02
26	28	100.0	327	1	S26693	transcription factor	6.56e+02
27	28	100.0	352	2	E71164	hypothetical protein	6.56e+02
28	28	100.0	354	2	A64894	hypothetical protein	6.56e+02
29	28	100.0	371	2	C70626	hypothetical protein	6.56e+02
30	28	100.0	412	2	F64849	probable permease b10	6.56e+02
31	28	100.0	417	2	S64006	hypothetical protein	6.56e+02
32	28	100.0	419	2	A70814	probable integral mem	6.56e+02
33	28	100.0	452	2	S77040	probable membrane pro	6.56e+02
34	28	100.0	504	2	S24314	bacterial leucyl amin	6.56e+02
35	28	100.0	551	2	S66701	hypothetical protein	6.56e+02
36	28	100.0	576	2	B71420	probable membrane pro	6.56e+02
37	28	100.0	591	2	D64204	membrane lipoprotein	6.56e+02
38	28	100.0	591	2	S64489	phosphoribosylaminoim	6.56e+02
39	28	100.0	685	2	S64985	hypothetical protein	6.56e+02
40	28	100.0	709	2	E64213	DNA topoisomerase (EC	6.56e+02
41	28	100.0	1048	2	C70626	NMD5 protein - yeast	6.56e+02
42	28	100.0	1150	2	S57155	NMD5 protein - yeast	6.56e+02
43	28	100.0	1671	2	B47114	phosphoprotein phosph	6.56e+02
44	28	100.0	1698	2	S51869	probable membrane pro	6.56e+02
45	28	100.0	2672	2	A48126	translation activator	6.56e+02

ALIGNMENTS

RESULT   1

ENTRY   S28565   #type complete
TITLE   hypothetical protein (Athb-2 5' region) - Arabidopsis
            thaliana
ORGANISM   #formal_name Arabidopsis thaliana #common_name mouse-ear
            cress
            #variety strain Columbia
DATE   12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
            24-Sep-1998
ACCESSIONS S28565; S31423
REFERENCE   S28565
  #authors Carabelli, M.; Sessa, G.; Baima, S.; Morelli, G.; Ruberti, I.
  #journal Plant J. (1993) 4:469-479
  #title   The Arabidopsis Athb-2 and -4 genes are strongly induced by
            far-red-rich light.
  #cross-references MUID:94035194
  #accession S28565
            ##molecule_type mRNA
            ##residues 1-45 ##label CAR1
            ##cross-references EMBL:X68145; NID:g16178; PID:g16179
  #accession S31423
            ##molecule_type DNA
            ##residues 1-45 ##label CAR2
            ##cross-references EMBL:X68146; NID:g16330; PID:g16331
SUMMARY   #length 45 #molecular-weight 5101 #checksum 1089

      Query Match   100.0%; Score 28; DB 2; Length 45;
      Best Local Similarity   100.0%;
      Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   31 LSASL 35
              |||||
Db   8 LSASL 12

RESULT   2

ENTRY   S38564   #type fragment
TITLE   Ig kappa chain V region (ASW1) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
            20-Mar-1998
ACCESSIONS S38564
REFERENCE   S38559
  #authors Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
  #submission submitted to the EMBL Data Library, September 1993
  #description Molecular analysis of mercury-induced anti-nucleolar
            antibodies in H-2s mice.
```

```
#accession          S38564
##status            preliminary
##molecule_type     mRNA
##residues          1-93 ##label MON
##cross-references  EMBL:X75105; NID:g414153; PID:g414154
CLASSIFICATION
  #superfamily      immunoglobulin
KEYWORDS            immunoglobulin V region; Immunoglobulin homology
SUMMARY             #length 93 #checksum 1511
```

Query Match
Best Local Similarity 100.0%;   Score 28; DB 2; Length 93;
Matches   5; Conservative   0; Pred. No. 6.56e+02; Mismatches   0; Indels   0; Gaps   0;

```
Db   11  LSASL  15
         |||||
Qy   31  LSASL  35
```

RESULT 3

```
ENTRY               S50530
TITLE               hypothetical protein YEL059w - yeast (Saccharomyces
                    cerevisiae)
ORGANISM            #formal_name Saccharomyces cerevisiae
DATE                28-May-1993 #sequence_revision 24-Feb-1995 #text_change
                    21-Nov-1997
ACCESSIONS          S50530
                    S50428
REFERENCE           S50530
  #authors          Dietrich, F.S.
  #submission       submitted to the EMBL Data Library, December 1994
  #description      The sequence of S. cerevisiae cosmids 9669, 8334, 8199, and
                    lambda clone 1160.
  #accession        S50530
    ##molecule_type DNA
    ##residues      1-102 ##label DIE
  #cross-references EMBL:U18795; NID:g603241; PID:g603259; MIPS:YEL059w
GENETICS
  #map_position     5L
SUMMARY             #length 102 #molecular-weight 11341 #checksum 6268
```

Query Match
Best Local Similarity 100.0%;   Score 28; DB 2; Length 102;
Matches   5; Conservative   0; Pred. No. 6.56e+02; Mismatches   0; Indels   0; Gaps   0;

```
Db   70  LSASL  74
         |||||
Qy   31  LSASL  35
```

RESULT 4

```
ENTRY               C33936          #type fragment
TITLE               Ig kappa chain V region (VM113) - mouse (fragment)
ORGANISM            #formal_name Mus musculus #common_name house mouse
DATE                09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
                    08-Sep-1997
ACCESSIONS          C33936
                    A33936
REFERENCE           A33936
  #authors          Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
  #journal          Proc. Natl. Acad. Sci. U.S.A. (1989) 86:4664-4668
  #title            Nucleotide changes in sequential variants of influenza virus
                    hemagglutinin genes and molecular structures of
                    corresponding monoclonal antibodies specific for each
                    variant.
  #cross-references MUID:89282831
  #accession        C33936
    ##status        preliminary
    ##molecule_type mRNA
    ##residues      1-106 ##label MEE
  #cross-references GB:J04577; NID:g623187; PID:g623189
CLASSIFICATION      #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS            heterotetramer; immunoglobulin
SUMMARY             #length 106 #checksum 2278
```

Query Match
100.0%;   Score 28; DB 2; Length 106;

RESULT 5

```
ENTRY               PL0259          #type fragment
TITLE               Ig kappa chain V region (anti-DNA, DP1VK) - mouse (fragment)
ORGANISM            #formal_name Mus musculus #common_name house mouse
DATE                16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
REFERENCE           PL0259
ACCESSIONS          PL0259
  #authors          Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
                    D.; Marshak-Rothstein, A.; Weigert, M.
  #journal          J. Exp. Med. (1990) 171:265-297
  #title            Anti-DNA antibodies from autoimmune mice arise by clonal
                    expansion and somatic mutation.
  #cross-references MUID:90111618
    ##molecule_type mRNA
    ##residues      1-106 ##label SHL
CLASSIFICATION      #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS            heterotetramer; immunoglobulin
SUMMARY             #length 106 #checksum 2162
FEATURE
     1-23           #region framework 1\
    24-34           #region complementarity-determining 1\
    35-49           #region framework 2\
    50-56           #region complementarity-determining 2\
    57-88           #region framework 3\
    89-97           #region complementarity-determining 3\
    98-106          #region framework 4
```

Query Match
Best Local Similarity 100.0%;   Score 28; DB 2; Length 106;
Matches   5; Conservative   0; Pred. No. 6.56e+02; Mismatches   0; Indels   0; Gaps   0;

```
Db   11  LSASL  15
         |||||
Qy   31  LSASL  35
```

RESULT 6

```
ENTRY               PL0260          #type fragment
TITLE               Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
ORGANISM            #formal_name Mus musculus #common_name house mouse
DATE                16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
REFERENCE           PL0260
ACCESSIONS          PL0260
  #authors          Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
                    D.; Marshak-Rothstein, A.; Weigert, M.
  #journal          J. Exp. Med. (1990) 171:265-297
  #title            Anti-DNA antibodies from autoimmune mice arise by clonal
                    expansion and somatic mutation.
  #cross-references MUID:90111618
    ##molecule_type mRNA
    ##residues      1-106 ##label SHL
CLASSIFICATION      #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS            heterotetramer; immunoglobulin
FEATURE
     1-23           #region framework 1\
    24-34           #region complementarity-determining 1\
    35-49           #region framework 2\
    50-56           #region complementarity-determining 2\
    57-88           #region framework 3\
    89-97           #region complementarity-determining 3\
    98-106          #region framework 4
```

SUMMARY #length 106 #checksum 2157-

Query Match 100.0%; Score 28; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 6.56e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15
          |||||
Qy 31 LSASL 35

RESULT 7

ENTRY B47271 #type fragment
TITLE nitrophenyl phosphonate-specific antibody 48G7 light chain VJ
        - synthetic (fragment)
ORGANISM Mus musculus (house mouse) gene engineered and expressed in
#note Escherichia coli
#formal_name synthetic
TITLE 21-Sep1993 #sequence_revision 11-Aug-1995 #text_change
DATE 11-Aug-1995
ACCESSIONS
REFERENCE B47271
        A47271
#authors Lesley, S.A.; Patten, P.A.; Schultz, P.G.
#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1160-1165
#title A genetic approach to the generation of antibodies with
        enhanced catalytic activities.
#cross-references MUID:93165660
#accession B47271
#molecule_type DNA; protein
##residues 1-108 ##label LES
##note sequence extracted from NCBI backbone (NCBIN:124856,
        NCBIP:124859)
##note parts of this sequence were determined by protein
        sequencing

FEATURE
24-89 #disulfide_bonds #status predicted
SUMMARY #length 108 #checksum 9036

Query Match 100.0%; Score 28; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.56e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 LSASL 16
          |||||
Qy 31 LSASL 35

RESULT 8

ENTRY C26405 #type complete
TITLE Ig kappa chain V region (3D10) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
        16-Aug-1996
ACCESSIONS
REFERENCE C26405
        A90518
#authors Smith, J.A.; Margolies, M.N.
#journal Biochemistry (1987) 26:604-612
#title Complete amino acid sequences of the heavy and light chain
        variable regions from two A/J mouse antigen nonbinding
        monoclonal antibodies bearing the predominant p-azophenyl
        arsonate idiotype.
#cross-references MUID:87157677
#accession C26405
#molecule_type protein
##residues 1-108 ##label SMI
##experimental_source strain A/J
CLASSIFICATION
KEYWORDS #superfamily immunoglobulin v region; immunoglobulin homology
        heterotetramer; immunoglobulin
SUMMARY #length 108 #molecular-weight 11944 #checksum 1684

Query Match 100.0%; Score 28; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.56e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15
          |||||
Qy 31 LSASL 35

Db 11 LSASL 15
          |||||
Qy 31 LSASL 35

RESULT 9

ENTRY B26405 #type complete
TITLE Ig kappa chain V region (1F6) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 16-Aug-1996
#authors 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change
#journal
#title
ACCESSIONS
REFERENCE B26405
        A90518
#authors Smith, J.A.; Margolies, M.N.
#journal Biochemistry (1987) 26:604-612
#title Complete amino acid sequences of the heavy and light chain
        variable regions from two A/J mouse antigen nonbinding
        monoclonal antibodies bearing the predominant p-azophenyl
        arsonate idiotype.
#cross-references MUID:87157677
#accession B26405
#molecule_type protein
##residues 1-108 ##label SMI
##experimental_source strain A/J
CLASSIFICATION
KEYWORDS #superfamily immunoglobulin v region; immunoglobulin homology
        heterotetramer; immunoglobulin
SUMMARY #length 108 #molecular-weight 11985 #checksum 1541

Query Match 100.0%; Score 28; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.56e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15
          |||||
Qy 31 LSASL 35

RESULT 10

ENTRY KVMS09 #type complete
TITLE Ig kappa chain V region (E109) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1988 #sequence_revision 30-Jun-1993 #text_change
        16-Aug-1996
ACCESSIONS
REFERENCE B92808; A01929
        A92808
#authors Vrana, M.; Rudikoff, S.; Potter, M.
#journal J. Immunol. (1979) 122:1905-1910
#title The structural basis of a hapten-inhibitable kappa-chain
        idiotype.
COMMENT This chain was isolated from a myeloma protein that binds inulin.
COMPLEX An immunoglobulin heterotetramer subunit consists of two
        identical light (kappa or lambda) and two identical heavy
        (alpha, delta, epsilon, gamma, or mu) chains usually
        stabilized by interchain disulfide bonds. In some cases,
        such as IgA and IgM, the subunits associate into larger
        oligomers.
#cross-references MUID:79195288
#accession B92808
#molecule_type protein
##residues 1-108 ##label VRA
CLASSIFICATION
KEYWORDS #superfamily immunoglobulin v region; immunoglobulin homology
        heterotetramer; immunoglobulin
FEATURE
23-88 #disulfide_bonds #status predicted
SUMMARY #length 108 #molecular-weight 11876 #checksum 6583

Query Match 100.0%; Score 28; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 6.56e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 LSASL 15
          |||||

Qy   31 LSASL 35

RESULT 11

ENTRY   KVMS82   #type complete
TITLE   Ig kappa chain V region (W3082) - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
               16-Aug-1996
ACCESSIONS   B92811; A01929
REFERENCE   A92811
               #authors Johnson, N.; Slankard, J.; Paul, L.; Hood, L.
               #journal J. Immunol. (1982) 128:302-307
               #title The complete V domain amino acid sequences of two myeloma
               inulin-binding proteins.
               #cross-references MUID:82099361
               #accession B92811
               ##molecule_type protein
               ##residues 1-108 #label JOH
COMPLEX   This chain was isolated from a myeloma protein that binds inulin.
               An immunoglobulin heterotetramer subunit consists of two
               identical light (kappa or lambda) and two identical heavy
               (alpha, delta, epsilon, gamma, or mu) chains usually
               stabilized by interchain disulfide bonds. In some cases,
               such as IgA and IgM, the subunits associate into larger
               oligomers.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
FEATURE
               23-88   #disulfide_bonds #status predicted
SUMMARY   #length 108 #molecular-weight 11850 #checksum 6696

Query Match   100.0%;   Score 28;   DB 1;   Length 109;
Best Local Similarity 100.0%;   Pred. No. 6.56e+02;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   11 LSASL 15
         |||||
Qy   31 LSASL 35

RESULT 12

ENTRY   S03521   #type fragment
TITLE   Ig kappa chain V region precursor V region (hybridoma PTF-02) - mouse
               (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
               29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
               08-Sep-1997
REFERENCE   S03521; S05066
               S03521
               #authors Adzhalov, V.A.; Stepchenko, A.G.; Deev, S.A.; Polyanovskii,
               O.L.
               #journal Mol. Biol. (1987) 21:945-948
               #title Structure of the variable gene coding for chi-chains of
               antibodies produced by hybridoma PTF-02.
               #accession S03521
               ##molecule_type DNA
               ##residues 1-124 #label ADZ
               ##cross-references EMBL:X07963; NID:g33645; PID:g33646
GENETICS   #introns 17/3
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin
KEYWORDS   heterotetramer; immunoglobulin
FEATURE
               1-17   #domain signal sequence #status predicted #label SIG\
               17-124   #product Ig kappa chain V region #status predicted
               1-17   #domain V segment #label MAT\
               17-113   #domain V segment #label VSE\
               114-124 #domain J segment #label JSE\
               40-105   #disulfide_bonds #status predicted
SUMMARY   #length 124 #checksum 9886

Query Match   100.0%;   Score 28;   DB 2;   Length 124;

Db   28 LSASL 32
         |||||
Qy   31 LSASL 35

Best Local Similarity 100.0%;   Pred. No. 6.56e+02;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 13

ENTRY   KVMSM4   #type complete
TITLE   Ig kappa chain precursor V region (MOPC 41) - mouse
CONTAINS   Ig kappa chain precursor V region VK41
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change
               16-Aug-1996
ACCESSIONS   A93211; B93211; A93815; A94239; A01922; A01923
REFERENCE   A93211
               #authors Seidman, J.G.; Max, E.E.; Leder, P.
               #journal Nature (1979) 280:370-375
               #title A kappa-immunoglobulin gene is formed by site-specific
               recombination without further somatic mutation.
               #cross-references MUID:79221900
               #accession A93211
               ##molecule_type DNA
               ##residues 1-130 #label PC41
               #accession B93211
               ##molecule_type DNA
               ##residues 1-117 #label VK41
               the sequences were determined from the differentiated
               gene MOPC 41 and the germline gene VK41
REFERENCE   A93815
               #authors Burstein, Y.; Schechter, I.
               #journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720
               #title Amino acid sequence of the NH-2-terminal extra piece segments
               of the precursors of mouse immunoglobulin lambda-1-type and
               kappa-type light chains.
               #cross-references MUID:77148916
               #accession A93815
               ##molecule_type protein
               ##residues 23-49,'B',51-53,'LSB',57-58,'22',61-62,'B2',65-76,'B',
               78-108,110-130 #label GRA
               #note Met-3 is apparently used as an alternative initiator in
               ##note 258 of the chains
COMPLEX   19/1
               An immunoglobulin heterotetramer subunit consists of two
               identical light (kappa or lambda) and two identical heavy
               (alpha, delta, epsilon, gamma, or mu) chains usually
               stabilized by interchain disulfide bonds. In some cases,
               such as IgA and IgM, the subunits associate into larger
               oligomers.
GENETICS   #experimental_source Bence Jones protein MOPC 41
REFERENCE   A94239
               #authors Gray, W.R.; Dreyer, W.J.; Hood, L.
               #journal Science (1967) 155:465-467
               #title Mechanism of antibody synthesis: size differences between
               mouse kappa chains.
               #cross-references MUID:67056897
               #accession A94239
               ##molecule_type protein
               ##residues 23-49,'B',51-53,'LSB',57-58,'22',61-62,'B2',65-76,'B',
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   alternative initiators; heterotetramer; immunoglobulin
FEATURE
               1-22   #domain signal sequence #status experimental #label
               SIG1\
               3-22   #domain signal sequence #status experimental #label
               SIG2\
               23-130   #product Ig kappa chain V region (MOPC 41) #status
               experimental #label MA1\
               38-112   #domain immunoglobulin homology #label IMM\
               45-110   #disulfide_bonds #status predicted
SUMMARY   #length 130 #molecular-weight 14311 #checksum 6707

```
SUMMARY            #length 165  #checksum 5256
Query Match        100.0%;  Score 28;  DB 2;  Length 165;
Best Local Similarity 100.0%;  Pred. No. 6.56e+02;
Matches  5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db      122 LSASL 126
            |||||
Qy       31 LSASL  35
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Search completed: Tue Apr 20 13:56:36 1999
Job time : 17 secs.

```
RESULT  14
ENTRY      B69465         #type complete
TITLE      transcription regulator AsnC family homolog - Archaeoglobus
           fulgidus
ORGANISM   #formal_name Archaeoglobus fulgidus
DATE       05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
           02-Jul-1998
ACCESSIONS A69250
REFERENCE  B69465
#authors   Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson,
           K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.;
           Peterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graham,
           D.E.; Kyrpides, N.C.; Fleischmann, R.D.; Quackenbush, J.;
           Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
           Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.;
           Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.;
           Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman,
           J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs,
           T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.;
           D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.;
           Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese,
           C.R.; Venter, J.C.
#journal   Nature (1997) 390:364-370
#title     The complete genome sequence of the hyperthermophilic,
           sulfate-reducing archaeon Archaeoglobus fulgidus.
#cross-references MUID:9804343
#accession B69465
##status   preliminary; nucleic acid sequence not shown;
           translation not shown
##molecule_type DNA
##residues 1-138  #label KLE
##cross-references GB:AE000984; GB:AE000782; NID:g2689307; PID:g2648831;
           TIGR:AF1723
SUMMARY            #length 138  #molecular-weight 15577  #checksum 3741
Query Match        100.0%;  Score 28;  DB 2;  Length 138;
Best Local Similarity 100.0%;  Pred. No. 6.56e+02;
Matches  5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db       61 LSASL  65
            |||||
Qy       31 LSASL  35
```

```
RESULT  15
ENTRY      JE0065         #type fragment
TITLE      retroviral proteinase-like protein - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
           24-Feb-1995
ACCESSIONS JE0065
REFERENCE  JE0065
#authors   Johansen, T.; Holm, T.; Bjorklid, E.
#journal   Gene (1989) 79:259-267
#title     Members of the RTVL-H family of human endogenous
           retrovirus-like elements are expressed in placenta.
#cross-references MUID:9006755
#accession JE0065
##molecule_type mRNA
##residues 1-165  #label JOH
##experimental_source placenta
##note     readthrough of the terminator TGA may occur between the
           codons GAT for 19-Asp and CGC for 20-Arg
```

```
Query Match        100.0%;  Score 28;  DB 1;  Length 130;
Best Local Similarity 100.0%;  Pred. No. 6.56e+02;
Matches  5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db       33 LSASL  37
            |||||
Qy       31 LSASL  35
```

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*                                                *
*          M P S R C H            (TM)           *
*                                                *
**************************************************
```

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Tue Apr 20 13:54:52 1999; MasPar time 2.29 Seconds
                 58.693 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-836-455-2
                  (31-35) from US08836455.pep (1 of 3)
Perfect Score: 28
Sequence: 1 LSASL 5

Scoring table: PAM 150
                  Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%
                  Listing first 45 summaries

Database: swiss-prot35
                  1:swissprot

Statistics: Mean 17.476; Variance 12.170; scale 1.436

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result   %   Query
No. Score Match Length DB ID   Description   Pred. No.
```

| Result No. | Score | % Match | Query Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 28 | 100.0 | 102 | 1 | YEG9_YEAST | HYPOTHETICAL 11.3 KD P | 3.19e+02 |
| 2 | 28 | 100.0 | 108 | 1 | KV5U_MOUSE | IG KAPPA CHAIN V-V REG | 3.19e+02 |
| 3 | 28 | 100.0 | 108 | 1 | KV5T_MOUSE | IG KAPPA CHAIN V-V REG | 3.19e+02 |
| 4 | 28 | 100.0 | 108 | 1 | KV5R_MOUSE | IG KAPPA CHAIN V-V REG | 3.19e+02 |
| 5 | 28 | 100.0 | 125 | 1 | MFAP_SACKL | MATING FACTOR ALPHA PR | 3.19e+02 |
| 6 | 28 | 100.0 | 180 | 1 | YFXK_BRAJA | HYPOTHETICAL PROTEIN I | 3.19e+02 |
| 7 | 28 | 100.0 | 255 | 1 | YFCA_HAEIN | HYPOTHETICAL PROTEIN H | 3.19e+02 |
| 8 | 28 | 100.0 | 303 | 1 | ARAL_STRAT | PUTATIVE ARAC-LIKE TRA | 3.19e+02 |
| 9 | 28 | 100.0 | 304 | 1 | ARAL_STRLI | PUTATIVE ARAC-LIKE TRA | 3.19e+02 |
| 10 | 28 | 100.0 | 317 | 1 | YN8F_YEAST | HYPOTHETICAL 35.4 KD P | 3.19e+02 |
| 11 | 28 | 100.0 | 365 | 1 | MEFB_HUMAN | MYOCYTE-SPECIFIC ENHAN | 3.19e+02 |
| 12 | 28 | 100.0 | 367 | 1 | YMCP_BPF41 | HYPOTHETICAL PROTEIN I | 3.19e+02 |
| 13 | 28 | 100.0 | 371 | 1 | LEU3_SCHPO | 3-ISOPROPYLMALATE DEHY | 3.19e+02 |
| 14 | 28 | 100.0 | 416 | 1 | MYC_CHICK | MYC PROTO-ONCOGENE PRO | 3.19e+02 |
| 15 | 28 | 100.0 | 416 | 1 | MYC_AVIOK | MYC TRANSFORMING PROTE | 3.19e+02 |
| 16 | 28 | 100.0 | 417 | 1 | YTFR_ECOLI | HYPOTHETICAL ABC TRANS | 3.19e+02 |
| 17 | 28 | 100.0 | 417 | 1 | YGA4_YEAST | HYPOTHETICAL 46.4 KD T | 3.19e+02 |
| 18 | 28 | 100.0 | 421 | 1 | MYC_AVIM2 | MYC TRANSFORMING PROTE | 3.19e+02 |
| 19 | 28 | 100.0 | 422 | 1 | MYC_AVIMC | MYC TRANSFORMING PROTE | 3.19e+02 |
| 20 | 28 | 100.0 | 422 | 1 | MYC_AVIMD | MYC TRANSFORMING PROTE | 3.19e+02 |
| 21 | 28 | 100.0 | 443 | 1 | PORD_PSEAE | PORIN D PRECURSOR (OUT | 3.19e+02 |
| 22 | 28 | 100.0 | 458 | 1 | NU4M_PETMA | NADH-UBIQUINONE OXIDOR | 3.19e+02 |
| 23 | 28 | 100.0 | 479 | 1 | 6PGD_TRYBB | 6-PHOSPHOGLUCONATE DEH | 3.19e+02 |
| 24 | 28 | 100.0 | 489 | 1 | TCPC_VIBCH | TOXIN CORREGULATED PIL | 3.19e+02 |
| 25 | 28 | 100.0 | 518 | 1 | YX23_CAEEL | HYPOTHETICAL 59.7 KD P | 3.19e+02 |
| 26 | 28 | 100.0 | 529 | 1 | 2ACB_HUMAN | PROTEIN PHOSPHATASE PP | 3.19e+02 |
| 27 | 28 | 100.0 | 533 | 1 | CAG2_MOUSE | BETA-1,4 N-ACETYLGALAC | 3.19e+02 |
| 28 | 28 | 100.0 | 648 | 1 | VE1_PCPV1 | REPLICATION PROTEIN E1 | 3.19e+02 |
| 29 | 28 | 100.0 | 680 | 1 | NOLO_RHISN | NODULATION PROTEIN NOL | 3.19e+02 |
| 30 | 28 | 100.0 | 709 | 1 | TOP1_MYCGE | DNA TOPOISOMERASE I (E | 3.19e+02 |
| 31 | 28 | 100.0 | 725 | 1 | AREA_PENCH | NITROGEN REGULATORY PR | 3.19e+02 |
| 32 | 28 | 100.0 | 827 | 1 | MOF_DROME | MALES-ABSENT ON THE FI | 3.19e+02 |
| 33 | 28 | 100.0 | 842 | 1 | AMPN_LACDL | AMINOPEPTIDASE N (EC 3 | 3.19e+02 |
| 34 | 28 | 100.0 | 860 | 1 | AREA_PENRO | NITROGEN REGULATORY PR | 3.19e+02 |
| 35 | 28 | 100.0 | 865 | 1 | NRFA_PENUR | NITROGEN REGULATORY PR | 3.19e+02 |
| 36 | 28 | 100.0 | 870 | 1 | YSO5_CAEEL | HYPOTHETICAL 98.0 KD P | 3.19e+02 |
| 37 | 28 | 100.0 | 876 | 1 | AREA_EMENI | NITROGEN REGULATORY PR | 3.19e+02 |
| 38 | 28 | 100.0 | 882 | 1 | AREA_ASPNG | NITROGEN REGULATORY PR | 3.19e+02 |
| 39 | 28 | 100.0 | 925 | 1 | PWP2_CAEEL | PERIODIC TRYPTOPHAN PR | 3.19e+02 |
| 40 | 28 | 100.0 | 925 | 1 | PUR2_MOUSE | PHOSPHORIBOSYLAMINE--G | 3.19e+02 |
| 41 | 28 | 100.0 | 1010 | 1 | ATHA_HUMAN | POTASSIUM-TRANSPORTING | 3.19e+02 |
| 42 | 28 | 100.0 | 1035 | 1 | NMD5_YEAST | NONSENSE-MEDIATED MRNA | 3.19e+02 |
| 43 | 28 | 100.0 | 1048 | 1 | 2ACA_HUMAN | PROTEIN PHOSPHATASE PP | 3.19e+02 |
| 44 | 28 | 100.0 | 1150 | 1 | YK76_YEAST | HYPOTHETICAL 137.5 KD | 3.19e+02 |
| 45 | 28 | 100.0 | 1195 | 1 | A2MG_RAT | ALPHA-2-MACROGLOBULIN | 3.19e+02 |
| | | 100.0 | 1472 | 1 | | | 3.19e+02 |

ALIGNMENTS

```
RESULT 1
ID   YEG9_YEAST     STANDARD;      PRT;   102 AA.
AC   P39982;
DT   01-FEB-1995 (REL. 31, CREATED)
DT   01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 11.3 KD PROTEIN IN SOM1-PCM1 INTERGENIC REGION.
GN   YEL059W.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
     [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288C / AB972;
RA   DIETRICH F.S., MULLIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R.,
RA   AVILES E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M.,
RA   CHUNG E., DUNCAN M., GUZMAN E., HARTZELL G., HUNICKE-SMITH S.,
RA   HYMAN R., KAYSER A., KOMP C., LASHKARI D., LEW H., LIN D.,
RA   MOSEDALE D., NAKAHARA K., NAMATH A., NORGREN R., OEFNER P., OH C.,
RA   PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN T., SMITH V.,
RA   TAYLOR P., WEI Y., YELTON M., BOTSTEIN D., DAVIS R.W.;
RL   SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
KW   HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
FT   TRANSMEM      18     38       POTENTIAL.
FT   TRANSMEM      70     90       POTENTIAL.
SQ   SEQUENCE   102 AA;  11341 MW;  5AB0614B CRC32;

Query Match                         Score 28;  DB 1;  Length 102;
Best Local Similarity 100.0%;                  Pred. No. 3.19e+02;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db    70 LSASL 74
         |||||
Qy    31 LSASL 35

RESULT 2
ID   KV5U_MOUSE     STANDARD;      PRT;   108 AA.
AC   P04946;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (NQ5-89.4).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 83271467.
RA   KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;
RL   NATURE 304:320-324(1983).
CC   -!- ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
DR   EMBL; K00745; G194455; -.
     HSSP; P01607; 1PAI.
KW   IMMUNOGLOBULIN V REGION; HYBRIDOMA.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;    11866 MW;  D396F142 CRC32;

Qy          31  LSASL  35

Query Match             100.0%;  Score 28;  DB 1;  Length 108;
Best Local Similarity   100.0%;  Pred. No. 3.19e+02;
  Matches    5;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db          11  LSASL  15
                |||||
            31  LSASL  35


RESULT 3
ID   KV5T_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01653;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   -!- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND
     BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 82099361.
RA   JOHNSON N., SLANKARD J., PAUL L., HOOD L.;
RL   J. IMMUNOL. 128:302-307(1982).
     PIR; B92811; KVMS82.
DR   HSSP; P01607; 1FVD.
     IMMUNOGLOBULIN V REGION.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    108       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;    11850 MW;  6CA5F4A0 CRC32;

Qy          31  LSASL  35

Query Match             100.0%;  Score 28;  DB 1;  Length 108;
Best Local Similarity   100.0%;  Pred. No. 3.19e+02;
  Matches    5;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db          11  LSASL  15
                |||||
            31  LSASL  35


RESULT 4
ID   KV5R_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01651;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
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DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (EPC 109).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RP   SEQUENCE.
RN   [1]
RX   MEDLINE; 79195288.
RA   VRANA M., RUDIKOFF S., POTTER M.;
RL   J. IMMUNOL. 122:1905-1910(1979).
CC   -!- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND
CC       BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
     PIR; B92808; KVMS09.
HSSP; P01607; 1FVD.
KW   IMMUNOGLOBULIN V REGION.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    108       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE    108 AA;    11876 MW;  3B5013E3 CRC32;

Qy          31  LSASL  35

Query Match             100.0%;  Score 28;  DB 1;  Length 108;
Best Local Similarity   100.0%;  Pred. No. 3.19e+02;
  Matches    5;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db          11  LSASL  15
                |||||
            31  LSASL  35


RESULT 5
ID   MFAP_SACKL     STANDARD;      PRT;   125 AA.
AC   P06648;
DT   01-JAN-1988 (REL. 06, CREATED)
DT   01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   MATING FACTOR ALPHA PRECURSOR (ALPHA MATING PHEROMONE).
OS   SACCHAROMYCES KLUYVERI (YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IFO 1894;
RX   MEDLINE; 87316894.
RA   EGEL-MITANI M., HANSEN M.T.;
RL   NUCLEIC ACIDS RES. 15:6303-6303(1987).
DR   EMBL; Y00385; G4859; -.
     PIR; A29120; A29120.
KW   PHEROMONE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     22
FT   CHAIN        23    125       ALPHA-MATING PHEROMONE.
FT   PEPTIDE      92    104       MATING FACTOR ALPHA.
FT   PEPTIDE     113    125       MATING FACTOR ALPHA (1ST COPY).
FT   CARBOHYD     57     57       POTENTIAL.
FT   CARBOHYD     67     67       POTENTIAL.
FT                                MATING FACTOR ALPHA (2ND COPY).
SQ   SEQUENCE    125 AA;    13925 MW;  F1214IF8 CRC32;

Qy          31  LSASL  35

Query Match             100.0%;  Score 28;  DB 1;  Length 125;
Best Local Similarity   100.0%;  Pred. No. 3.19e+02;
  Matches    5;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db           7  LSASL  11
                |||||
            31  LSASL  35


RESULT 6
ID   YFXK_BRAJA     STANDARD;      PRT;   180 AA.
AC   P29285;
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DT   01-DEC-1992 (REL. 24, CREATED)
DT   01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
DT   01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL PROTEIN IN FIXK 5'REGION (FRAGMENT).
OS   BRADYRHIZOBIUM JAPONICUM.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC   RHIZOBIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=110SPC4;
RX   MEDLINE; 92202135.
RA   ANTHAMATTEN D., SCHERB B., HENNECKE H.;
RL   J. BACTERIOL. 174:2111-2120(1992).
DR   EMBL; M86805; G152086; -.
DR   PIR; A42371; A42371.
KW   HYPOTHETICAL PROTEIN.
FT   NON_TER       1      1
SQ   SEQUENCE   180 AA;  19419 MW;  30B80FFA CRC32;

Qy    31 LSASL 35
      |||||
Db    31 LSASL 35

Query Match             100.0%;  Score 28;  DB 1;  Length 180;
Best Local Similarity   100.0%;  Pred. No. 3.19e+02;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


RESULT 7
ID   YFCA_HAEIN    STANDARD;    PRT;    255 AA.
AC   P46490;
DT   01-NOV-1995 (REL. 32, CREATED)
DT   01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL PROTEIN HI0198.
GN   HI0198.
OS   HAEMOPHILUS INFLUENZAE.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   PASTEURELLACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RD / KW20;
RX   MEDLINE; 95350630.
RA   FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA   KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
RA   MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
RA   SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
RA   WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
RA   UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
RA   FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
RA   GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
RA   VENTER J.C.;
RL   SCIENCE 269:496-512(1995).
RN   [2]
RP   REVISIONS.
RA   WHITE O., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
RL   SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC   -!- SIMILARITY: STRONG, TO E.COLI YFCA.
CC   -!- SIMILARITY: TO M.LEPRAE U1177B.
DR   EMBL; U32705; G1573158; -.
DR   TIGR; HI0198; -.
KW   HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
FT   TRANSMEM       7     27       POTENTIAL.
FT   TRANSMEM      28     48       POTENTIAL.
FT   TRANSMEM      76     96       POTENTIAL.
FT   TRANSMEM      99    119       POTENTIAL.
FT   TRANSMEM     132    152       POTENTIAL.
FT   TRANSMEM     153    173       POTENTIAL.
FT   TRANSMEM     191    211       POTENTIAL.
FT   TRANSMEM     235    255       POTENTIAL.
SQ   SEQUENCE   255 AA;  27608 MW;  E5E7023A CRC32;
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Qy    31 LSASL 35
      |||||
Db    59 LSASL 63

Query Match             100.0%;  Score 28;  DB 1;  Length 255;
Best Local Similarity   100.0%;  Pred. No. 3.19e+02;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


RESULT 8
ID   ARAL_STRAT    STANDARD;    PRT;    303 AA.
AC   Q03320;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   PUTATIVE ARAC-LIKE TRANSCRIPTION REGULATOR.
OS   STREPTOMYCES ANTIBIOTICUS.
OC   PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IMRU 3720;
RX   MEDLINE; 93194813.
RA   YU T.-W., CHEN C.W.;
RL   J. BACTERIOL. 175:1847-1852(1993).
CC   -!- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
CC       REGULATORS.
DR   EMBL; M96551; G153392; -.
DR   PIR; B47089; B47089.
DR   PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR   PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW   TRANSCRIPTION REGULATION; DNA-BINDING.
FT   DNA_BIND     218    237       H-T-H MOTIF (BY SIMILARITY).
SQ   SEQUENCE   303 AA;  32309 MW;  1BE5603C CRC32;

Qy    31 LSASL 35
      |||||
Db    17 LSASL 21

Query Match             100.0%;  Score 28;  DB 1;  Length 303;
Best Local Similarity   100.0%;  Pred. No. 3.19e+02;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


RESULT 9
ID   ARAL_STRLI    STANDARD;    PRT;    304 AA.
AC   P35319;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   PUTATIVE ARAC-LIKE TRANSCRIPTION REGULATOR.
OS   STREPTOMYCES LIVIDANS.
OC   PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=66 / 1326; TRANSPOSON=TN4811;
RX   MEDLINE; 93077460.
RA   CHEN C.W., YU T.-W., CHUNG H.-M., CHOU C.-F.;
RL   J. BACTERIOL. 174:7762-7769(1992).
CC   -!- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
CC       REGULATORS.
DR   EMBL; Z11519; G581707; -.
DR   PIR; E45277; E45277.
DR   PIR; S19843; S19843.
DR   PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
DR   PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KW   TRANSCRIPTION REGULATION; DNA-BINDING; TRANSPOSABLE ELEMENT.
FT   DNA_BIND     218    237       H-T-H MOTIF (BY SIMILARITY).
SQ   SEQUENCE   304 AA;  32878 MW;  6A9C2133 CRC32;

Qy    31 LSASL 35
      |||||
Db    17 LSASL 21

Query Match             100.0%;  Score 28;  DB 1;  Length 304;
Best Local Similarity   100.0%;  Pred. No. 3.19e+02;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Db       17 LSASL 21
            |||||
Qy       31 LSASL 35

RESULT 10
ID   YN8F_YEAST     STANDARD;      PRT;   317 AA.
AC   P53727;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 35.4 KD PROTEIN IN SEC12-SSK2 INTERGENIC REGION.
GN   YNR027W OR N3250.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   POHL T.M.;
RL   SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SIMILARITY: TO OTHER PYRIDOXINE KINASES.
CC   -!- CATALYTIC ACTIVITY: ATP + PYRIDOXAL = ADP + PYRIDOXAL 5'-
CC       PHOSPHATE.
DR   EMBL; Z71642; E239585; -.
KW   HYPOTHETICAL PROTEIN; TRANSFERASE; KINASE.
SQ   SEQUENCE 317 AA; 35367 MW; 3A4ADB04 CRC32;

Qy       31 LSASL 35

Query Match          100.0%;  DB 1;  Length 317;
Best Local Similarity 100.0%;  Pred. No. 3.19e+02;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db      254 LSASL 258
            |||||
Qy       31 LSASL 35
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RESULT 11
ID   MEF2_HUMAN     STANDARD;      PRT;   365 AA.
AC   Q02080;
DT   01-NOV-1995 (REL. 32, CREATED)
DT   01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT   15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE   MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE
DE   PROTEIN 2) (XMEF2) (RSRFR2).
GN   MEF2B OR XMEF2.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART, AND SKELETAL MUSCLE;
RX   MEDLINE; 92387551.
RA   YU Y.-T., BREITBART R.E., SMOOT L.B., LEE Y., MAHDAVI V.,
RA   NADAL-GINARD B.;
RL   GENES DEV. 6:1783-1798(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 9208105.
RA   POLLOCK R., TREISMAN R.;
RL   GENES DEV. 5:2327-2341(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   LAMERDIN J.E.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: TRANSCRIPTION FACTOR WHICH BINDS SPECIFICALLY TO THE
CC       MEF2 ELEMENT PRESENT IN THE REGULATORY REGIONS OF MANY MUSCLE-
CC       SPECIFIC GENES. ACTIVATES TRANSCRIPTION VIA THIS ELEMENT. MAY BE
CC       INVOLVED IN MUSCLE-SPECIFIC AND/OR GROWTH FACTOR-RELATED
CC       TRANSCRIPTION.
CC   -!- SUBUNIT: HETERODIMER.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL AND CARDIAC MUSCLE AND
CC       BRAIN.
CC   -!- SIMILARITY: BELONGS TO THE MEF2 SUBFAMILY OF MADS PROTEINS.
CC   -!- SIMILARITY: CONTAINS A DOMAIN FOUND IN SRF-TYPE TRANSCRIPTION
CC       FACTORS (MADS-DOMAIN).
DR   EMBL; X68502; G37992; -.
DR   EMBL; X63380; G36169; -.
DR   MIM; 600661; -.
DR   EMBL; AC002126; G2329909; -.
DR   PROSITE; PS00350; MADS_BOX_1; 1.
DR   PROSITE; PS50066; MADS_BOX_2; 1.
KW   TRANSCRIPTION REGULATION; NUCLEAR PROTEIN; DNA-BINDING; ACTIVATOR;
KW   MULTIGENE FAMILY.
FT   DOMAIN        3     57   MADS.
FT   DNA_BIND     58     86   MEF2-TYPE (POTENTIAL).
FT   DOMAIN        4     31   LYS-RICH (BASIC).
SQ   SEQUENCE 365 AA; 38638 MW; 59008C81 CRC32;

Qy       31 LSASL 35

Query Match          100.0%;  DB 1;  Length 365;
Best Local Similarity 100.0%;  Pred. No. 3.19e+02;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db      283 LSASL 287
            |||||
Qy       31 LSASL 35
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RESULT 12
ID   YMCP_BPF41     STANDARD;      PRT;   367 AA.
AC   P26812;
DT   01-AUG-1992 (REL. 23, CREATED)
DT   01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT   01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL PROTEIN IN MCP 3' REGION (FRAGMENT).
OS   LACTOCOCCUS LACTIS BACTERIOPHAGE F4-1.
OC   VIRIDAE; NOT YET CLASSIFIED.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91285421.
RA   CHUNG D.K., KIM J.H., BATT C.A.;
RL   GENE 101:121-125(1991).
DR   EMBL; M37979; -; NOT_ANNOTATED_CDS.
DR   PIR; PE04001; PE04001.
KW   HYPOTHETICAL PROTEIN.
FT   NON_TER     367    367
SQ   SEQUENCE 367 AA; 39163 MW; FBD3D6E5 CRC32;

Qy       31 LSASL 35

Query Match          100.0%;  DB 1;  Length 367;
Best Local Similarity 100.0%;  Pred. No. 3.19e+02;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db      293 LSASL 297
            |||||
Qy       31 LSASL 35
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RESULT 13
ID   LEU3_SCHPO     STANDARD;      PRT;   371 AA.
AC   P18869;
DT   01-NOV-1990 (REL. 16, CREATED)
DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   3-ISOPROPYLMALATE DEHYDROGENASE (EC 1.1.1.85) (BETA-IPM DEHYDROGENASE)
DE   (IMDH) (3-IPM-DH).
GN   LEU1.
OS   SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89106270.
RA   KIKUCHI Y., KITAZAWA Y., SHIMATAKE G., YAMAMOTO M.;
RL   CURR. GENET. 14:375-379(1988).
CC   -!- CATALYTIC ACTIVITY: 3-CARBOXY-2-HYDROXY-4-METHYLPENTANOATE +
CC       NAD(+) = 3-CARBOXY-4-METHYL-2-OXOPENTANOATE + NADH (THE PRODUCT
CC       DECARBOXYLATES TO 4-METHYL-2-OXOPENTANOATE).
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CC   -!- PATHWAY: THIRD STEP IN LEUCINE BIOSYNTHESIS.
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC   -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC       DEHYDROGENASES FAMILY.
DR   EMBL; M35910; G173412; -.
DR   HSSP; P00351; 1HEX.
DR   PROSITE; PS00470; IDH_IMDH; 1.
KW   OXIDOREDUCTASE; LEUCINE BIOSYNTHESIS; NAD.
SQ   SEQUENCE 371 AA; 39732 MW; DAEF72EA CRC32;

Query Match   100.0%;   Score 28;   DB 1;   Length 371;
Best Local Similarity 100.0%;   Pred. No. 3.19e+02;
Matches   5;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Db   308 LSASL 312
         |||||
Qy    31 LSASL 35


ID   MYC_AVIOK    STANDARD;    PRT;    416 AA.
AC   P12523;
DT   01-OCT-1989 (REL. 12, CREATED)
DT   01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
DT   01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE   MYC TRANSFORMING PROTEIN.
GN   V-MYC.
OS   AVIAN RETROVIRUS OK10.
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC   ONCOVIRINAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85190568.
RA   HAYFLICK J., SEEBURG P.H., OHLSSON R., PFEIFER-OHLSSON S.,
RA   WATSON D., PAPAS T., DUESBERG P.H.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 82:2718-2722(1985).
CC   -!- THIS PROTEIN IS SYNTHESIZED AS A GAG-MYC POLYPROTEIN.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE MYC FAMILY OF HELIX-LOOP-HELIX
CC       TRANSCRIPTION FACTORS.
DR   EMBL; M11352; G209657; -.
DR   PIR; A22669; TVFVAC.
DR   PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
KW   TRANSFORMING PROTEIN; NUCLEAR PROTEIN; DNA-BINDING; ONCOGENE.
FT   DNA_BIND    331    384    HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
SQ   SEQUENCE    416 AA;    46040 MW;    7040632F CRC32;

Query Match   100.0%;   Score 28;   DB 1;   Length 416;
Best Local Similarity 100.0%;   Pred. No. 3.19e+02;
Matches   5;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Db   3 LSASL 7
       |||||
Qy  31 LSASL 35


RESULT   15
ID   MYC_CHICK    STANDARD;    PRT;    416 AA.
AC   P01109;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   MYC PROTO-ONCOGENE PROTEIN (C-MYC).
GN   MYC.
OS   GALLUS GALLUS (CHICKEN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC   GALLIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 83169838.
RA   WATSON D.K., REDDY E.P., DUESBERG P.H., PAPAS T.S.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 80:2146-2150(1983).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 88302180.
RA   HAHN M., HAYWARD W.;
RL   MOL. CELL. BIOL. 8:2659-2662(1988).
RN   [3]
RP   SEQUENCE OF 1-44 FROM N.A.
RX   MEDLINE; 84272700.
RA   SHIH C.-K., LINIAL M., GOODENOW M.M., HAYWARD W.S.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 81:4697-4701(1984).
CC   -!- FUNCTION: PARTICIPATES IN THE REGULATION OF GENE TRANSCRIPTION.
CC       BINDS DNA BOTH IN A NON-SPECIFIC MANNER AND ALSO SPECIFICALLY TO
CC       RECOGNIZES THE CORE SEQUENCE CAC[GA]TG. SEEMS TO ACTIVATE THE
CC       TRANSCRIPTION OF GROWTH-RELATED GENES.
CC   -!- SUBUNIT: BINDS DNA AS AN HETERODIMER WITH MAX.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- DISEASE: OVEREXPRESSION OF C-MYC IS IMPLICATED IN THE ETIOLOGY OF
CC       A VARIETY OF HEMATOPOIETIC TUMORS.
CC   -!- SIMILARITY: TO OTHER MEMBERS OF THE MYC FAMILY OF HELIX-LOOP-HELIX
CC       TRANSCRIPTION FACTORS.
DR   EMBL; J00889; G212355; -.
DR   EMBL; M20006; G211566; -.
DR   PIR; A01352; FOCH.
DR   TRANSFAC; T00141; -.
DR   PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
KW   PROTO-ONCOGENE; NUCLEAR PROTEIN; DNA-BINDING; PHOSPHORYLATION;
KW   TRANSCRIPTION REGULATION; ACTIVATOR; GLYCOPROTEIN.
FT   DOMAIN      26     30    POLY-GLU.
FT   DOMAIN     163    167    POLY-PRO.
FT   DOMAIN     183    186    POLY-ALA.
FT   DOMAIN     398    401    POLY-ARG.
FT   DNA_BIND   331    384    HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT   CARBOHYD    61     61    GLCNAC (BY SIMILARITY).
SQ   SEQUENCE    416 AA;    46040 MW;    D761BBCB CRC32;

Query Match   100.0%;   Score 28;   DB 1;   Length 416;
Best Local Similarity 100.0%;   Pred. No. 3.19e+02;
Matches   5;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Db   3 LSASL 7
       |||||
Qy  31 LSASL 35

Search completed: Tue Apr 20 13:55:00 1999
Job time : 8 secs.
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MPSRCH (TM)

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 20 13:55:19 1999; MasPar time 4.54 Seconds
                                           54.879 Million cell updates/sec

Tabular output not generated.

Title: >US-08-836-455-2, from US08836455.pep (1 of 3)
Description: (31-35), from US08836455.pep (1 of 3)
Perfect Score: 28
Sequence: 1 LSASL 5

Scoring table: PAM 150
               Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: sptrembl6
               1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
               5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
               9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
               13:sp_vertebrate 14:sp_virus

Statistics: Mean 16.819; Variance 13.365; scale 1.258

               Pred. No. is the number of results predicted by chance to have a
               score greater than or equal to the score of the result being printed,
               and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	28	100.0	45	10	Q05480	HYPOTHETICAL 5.1 KD P	7.03e+02
2	28	100.0	132	14	O02180	HYPOTHETICAL 14.0 KD P	7.03e+02
3	28	100.0	138	1	O28551	HSDM, HSDS & HSDR GENE	7.03e+02
4	28	100.0	154	2	P74274	TRANSCRIPTIONAL REGULA	7.03e+02
5	28	100.0	166	4	Q15408	HYPOTHETICAL 17.5 KD P	7.03e+02
6	28	100.0	182	1	O57725	NEUTRAL PROTEASE LARGE	7.03e+02
7	28	100.0	204	11	O64015	182AA LONG HYPOTHETICA	7.03e+02
8	28	100.0	212	2	O28986	LEUKEMIA INHIBITORY FA	7.03e+02
9	28	100.0	221	1	O26628	CONSERVED HYPOTHETICAL	7.03e+02
10	28	100.0	241	11	P97771	HYPOTHETICAL 23.4 KD P	7.03e+02
11	28	100.0	268	2	O67364	ANTI-CEA 79 SINGLE CHA	7.03e+02
12	28	100.0	286	1	O28505	HYPOTHETICAL 30.4 KD P	7.03e+02
13	28	100.0	307	3	Q07534	DIPEPTIDE ABC TRANSPOR	7.03e+02
14	28	100.0	328	11	Q60458	ORF YDL119C	7.03e+02
15	28	100.0	340	2	O32253	CATIONIC AMINO ACID TR	7.03e+02
16	28	100.0	350	2	P95503	YVBQ PROTEIN.	7.03e+02
17	28	100.0	352	1	O58250	CHLOROPHYLL A/B ANTENN	7.03e+02
18	28	100.0	354	2	P77171	352AA LONG HYPOTHETICA	7.03e+02
19	28	100.0	357	3	O60137	FROM BASES 1485094 TO	7.03e+02
20	28	100.0	359	2	O66465	PHOSPHO-N-ACETYLMURAMO	7.03e+02
21	28	100.0	371	2	P96353	HYPOTHETICAL 40.2 KD P	7.03e+02
22	28	100.0	388	2	O32633	DAPE.	7.03e+02
23	28	100.0	417	2	P72417	HSDM, HSDS & HSDR GENE	7.03e+02
24	28	100.0	419	2	O53861	PUTATIVE MEMBRANE TRAN	7.03e+02
25	28	100.0	421	14	Q00089	MYC TRANSFORMING PROTE	7.03e+02
26	28	100.0	452	2	Q55962	HYPOTHETICAL 48.0 KD P	7.03e+02
27	28	100.0	505	3	O59785	HYPOTHETICAL 56.8 KD P	7.03e+02
28	28	100.0	587	14	O39279	COUNTERPART OF HSV-1 G	7.03e+02
29	28	100.0	652	11	O54858	CARBOXYPEPTIDASE 2.	7.03e+02
30	28	100.0	652	11	O54859	CARBOXYPEPTIDASE 2.	7.03e+02
31	28	100.0	694	3	Q07261	DNA FROM CHROMOSOME XI	7.03e+02
32	28	100.0	798	11	P97680	RIN1.	7.03e+02
33	28	100.0	875	14	O56221	P110.	7.03e+02
34	28	100.0	909	2	P74693	ACRIFLAVINE RESISTANCE	7.03e+02
35	28	100.0	934	4	O60622	PROTOCADHERIN 43.	7.03e+02
36	28	100.0	1006	2	O34073	ORF42.	7.03e+02
37	28	100.0	1094	14	O69025	DNA POLYMERASE (EC 2.7	7.03e+02
38	28	100.0	1107	14	O88919	RNA REPLICASE COMPONEN	7.03e+02
39	28	100.0	1144	14	P90356	129K PROTEIN.	7.03e+02
40	28	100.0	1196	10	O22476	BRASSINOSTEROID INSENS	7.03e+02
41	28	100.0	1271	2	O54504	MICROCYSTIN SYNTHETASE	7.03e+02
42	28	100.0	1295	2	O68900	PET PRECURSOR.	7.03e+02
43	28	100.0	1596	14	O66220	REPLICASE.	7.03e+02
44	28	100.0	1601	14	O88920	RNA REPLICASE READ-THR	7.03e+02
45	28	100.0	1648	14	P89877	186K PROTEIN.	7.03e+02

ALIGNMENTS

```
RESULT    1
ID   Q05480;
AC   Q05480;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 5.1 KD  PROTEIN IN ATHB-2 5'REGION.
OS   ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC   EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC   CAPPARALES; CRUCIFERAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=COLUMBIA;
RX   MEDLINE; 94035194.
RA   CARABELLI M., SESSA G., BAIMA S., MORELLI G., RUBERTI I.;
RL   PLANT J. 4:469-479(1993).
DR   EMBL; X68145; G16179; -.
DR   EMBL; X68146; G16331; -.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE 45 AA;  5101 MW;  F66824F4 CRC32;

Query Match             100.0%;  Score 28;  DB 10;  Length 45;
Best Local Similarity   100.0%;  Pred. No. 7.03e+02;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db          8 LSASL 12
              |||||
Qy         31 LSASL 35


RESULT    2
ID   O02180;
AC   O02180;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 14.0 KD PROTEIN.
OS   CHRISTONEURA FUMIFERANA NUCLEAR POLYHEDROSIS VIRUS (CFMNPV)
OC   VIRIDAE; DS-DNA ENVELOPED VIRUSES; BACULOVIRIDAE; EUBACULOVIRINAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IRELAND;
RA   POLUCHIENKO A., KRELL P.;
RL   SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

PRELIMINARY;     PRT;     132 AA.
```

DR   EMBL; U57401; G2062327; -.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE 132 AA; 13969 MW; 525B1B91 CRC32;

Query Match   100.0%;   Score 28; DB 14; Length 132;
Best Local Similarity 100.0%;   Pred. No. 7.03e+02;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   17 LSASL 21
        |||||
Qy   31 LSASL 35

RESULT 3
ID   O28551   PRELIMINARY;   PRT;   138 AA.
AC   O28551;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   TRANSCRIPTIONAL REGULATORY PROTEIN, ASNC FAMILY.
GN   AF1723.
OS   ARCHAEOGLOBUS FULGIDUS.
OC   ARCHAEA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE; 98049343.
RA   KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
RA   KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RA   RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
RA   FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA   KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA   PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
RA   OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
RA   COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
RA   SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA   MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA   VENTER J.C.;
RL   NATURE 390:364-370(1997).
DR   EMBL; AE000984; G2648831; -.
DR   TIGR; AF1723; -.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE 138 AA; 15577 MW; 9B383364 CRC32;

Query Match   100.0%;   Score 28; DB 1; Length 138;
Best Local Similarity 100.0%;   Pred. No. 7.03e+02;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   61 LSASL 65
        |||||
Qy   31 LSASL 35

RESULT 4
ID   P74274   PRELIMINARY;   PRT;   154 AA.
AC   P74274;
DT   01-FEB-1997 (TREMBLREL. 02, CREATED)
DT   01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 17.5 KD PROTEIN.
OS   SYNECHOCYSTIS SP.
OC   EUBACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PCC6803;
RA   TABATA S.;
RL   SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PCC6803;
RA   KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA   MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA   HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
RA   SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
RA   TABATA S.;
RL   DNA RES. 3:109-136(1996).
DR   EMBL; D90913; G1653454; -.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE 154 AA; 17497 MW; 1BB15C3A CRC32;

Query Match   100.0%;   Score 28; DB 2; Length 154;
Best Local Similarity 100.0%;   Pred. No. 7.03e+02;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   84 LSASL 88
        |||||
Qy   31 LSASL 35

RESULT 5
ID   Q15408   PRELIMINARY;   PRT;   166 AA.
AC   Q15408;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   NEUTRAL PROTEASE LARGE SUBUNIT (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 90067755.
RA   JOHANSEN T., HOLM T., BJORKLID E.;
RL   GENE 79:259-267(1989).
DR   EMBL; M27826; G804764; -.
DR   PFAM; PF00077; IVP.
KW   PROTEASE.
FT   NON_TER   1   1
SQ   SEQUENCE 166 AA; 17788 MW; 1DE57D18 CRC32;

Query Match   100.0%;   Score 28; DB 4; Length 166;
Best Local Similarity 100.0%;   Pred. No. 7.03e+02;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   123 LSASL 127
        |||||
Qy   31 LSASL 35

RESULT 6
ID   O57725   PRELIMINARY;   PRT;   182 AA.
AC   O57725;
DT   01-AUG-1998 (TREMBLREL. 07, CREATED)
DT   01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   182AA LONG HYPOTHETICAL PROTEIN.
GN   PHBD022.
OS   PYROCOCCUS HORIKOSHII.
OC   ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OT3;
RA   KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
RA   YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
RA   SAKAI M., OGURA K., OTSUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
RA   FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
RA   AOKI K., YOSHIZAWA T., NAKAMURA Y., MASUCHI Y., SHIZUYA H.,
RA   KIKUCHI H.;
RL   SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB009464; D1027108; -.
SQ   SEQUENCE 182 AA; 19120 MW; A4F6EDEC CRC32;

Query Match   100.0%;   Score 28; DB 1; Length 182;
Best Local Similarity 100.0%;   Pred. No. 7.03e+02;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   31 LSASL 35

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Db      175 LSASL 179
            |||||
Qy       31 LSASL 35
```

RESULT 7
```
ID   Q64015       PRELIMINARY;     PRT;   204 AA.
AC   Q64015;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   LEUKEMIA INHIBITORY FACTOR (LIF-LEUKEMIA INHIBITORY FACTOR).
GN   LIF.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94347086.
RA   HSU L.W., HEATH J.K.;
RL   BIOCHEM. J. 302:103-110(1994).
DR   EMBL; S73374; G663150; -.
DR   MGD; MGI:96787; LIF.
DR   PROSITE; PS00590; LIF_OSM; 1.
SQ   SEQUENCE  204 AA;  22485 MW;  8E590658 CRC32;

Query Match             100.0%;  Score 28;  DB 11;  Length 204;
Best Local Similarity   100.0%;  Pred. No. 7.03e+02;
Matches     5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Db      114 LSASL 118
            |||||
Qy       31 LSASL 35
```

RESULT 8
```
ID   O28986       PRELIMINARY;     PRT;   212 AA.
AC   O28986;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   CONSERVED HYPOTHETICAL PROTEIN.
GN   AF1282.
OS   ARCHAEOGLOBUS FULGIDUS.
OC   ARCHAEA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE; 98049343.
RA   KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
RA   KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RA   RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
RA   FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA   KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA   PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
RA   OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
RA   COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
RA   SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA   MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA   VENTER J.C.;
RL   NATURE 390:364-370(1997).
DR   EMBL; AE001016; G2649299; -.
DR   TIGR; AF1282; -.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE  212 AA;  24708 MW;  C3267F18 CRC32;

Query Match             100.0%;  Score 28;  DB 1;  Length 212;
Best Local Similarity   100.0%;  Pred. No. 7.03e+02;
Matches     5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Db      134 LSASL 138
            |||||
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Qy       31 LSASL 35
```

RESULT 9
```
ID   O26628       PRELIMINARY;     PRT;   221 AA.
AC   O26628;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 23.4 KD PROTEIN.
GN   MTH528.
OS   METHANOBACTERIUM THERMOAUTOTROPHICUM.
OC   ARCHAEA; EURYARCHAEOTA; METHANOBACTERIALES;
OC   METHANOBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DELTA H;
RX   MEDLINE; 98037514.
RA   SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
RA   ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
RA   HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
RA   SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
RA   JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
RA   MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA   DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
RL   J. BACTERIOL. 179:7135-7155(1997).
DR   EMBL; AE000836; G2621602; -.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE  221 AA;  23425 MW;  EF5A6F34 CRC32;

Query Match             100.0%;  Score 28;  DB 1;  Length 221;
Best Local Similarity   100.0%;  Pred. No. 7.03e+02;
Matches     5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Db       90 LSASL 94
            |||||
Qy       31 LSASL 35
```

RESULT 10
```
ID   P97771       PRELIMINARY;     PRT;   241 AA.
AC   P97771;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   CHUNG J.H., LEE S.D., YI K.S., SUH P.G., RYU S.H., CHOI S.J., KIM H.J.,
RA   KIM I.J., CHOI I.H., CHUNG H.K.;
RL   SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U88067; G1850548; -.
DR   PFAM; PF00047; ig.
FT   NON_TER       1      1
FT   NON_TER     241    241
SQ   SEQUENCE  241 AA;  26086 MW;  EBB2D29D CRC32;

Query Match             100.0%;  Score 28;  DB 11;  Length 241;
Best Local Similarity   100.0%;  Pred. No. 7.03e+02;
Matches     5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
Db      144 LSASL 148
            |||||
Qy       31 LSASL 35
```

RESULT 11
```
ID   O67364       PRELIMINARY;     PRT;   268 AA.
AC   O67364;
DT   01-AUG-1998 (TREMBLREL. 07, CREATED)
```

DT   01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 30.4 KD PROTEIN.
GN   AQ_1349.
OS   AQUIFEX AEOLICUS.
OC   EUBACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VF5;
RC   DECKERT G.
RA   DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RA   GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
RA   FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
RL   NATURE 392:353-358(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RL   SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   268 AA; 30387 MW; E6FF0262 CRC32;

Qy   31 LSASL 35

Db 246 LSASL 250

Query Match   100.0%; Score 28; DB 2; Length 268;
Best Local Similarity   100.0%; Pred. No. 7.03e+02;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 12
ID   028505   PRELIMINARY;   PRT;   286 AA.
AC   028505;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   DIPEPTIDE ABC TRANSPORTER, PERMEASE PROTEIN (DPPC).
GN   AF1769.
OS   ARCHAEOGLOBUS FULGIDUS.
OC   ARCHAEBACTERIA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
     MEDLINE: 98049343.
RA   KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON R.E.,
RA   KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.R., PETERSON J.D.,
RA   RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
RA   FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA   KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA   PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
RA   OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
RA   COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
RA   SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA   MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA   VENTER J.C.;
RL   NATURE 390:364-370(1997).
DR   EMBL; AE000080; G2648779; -.
DR   TIGR; AF1769; -.
DR   PFAM; PF00528; BPD_transp.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   286 AA; 30810 MW; BB200F80 CRC32;

Qy   31 LSASL 35
Db   91 LSASL 95

Query Match   100.0%; Score 28; DB 1; Length 286;
Best Local Similarity   100.0%; Pred. No. 7.03e+02;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 13
ID   Q07534   PRELIMINARY;   PRT;   307 AA.
AC   Q07534;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   ORF YDL119C.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   RIEGER M., MUELLER-AUER S., BRUECKNER M., SCHAEFER M., WAGNER G.;
RL   SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE FROM N.A.
RL   SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
     MIPS:
RL   SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC   INNER MEMBRANE (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR   EMBL; Z74167; E253042; -.
DR   PROSITE; PS00215; MITOCH_CARRIER.
DR   PFAM; PF00153; MITOCH_CARRIER; 2.
KW   MITOCHONDRION; REPEAT; TRANSMEMBRANE; TRANSPORT.
SQ   SEQUENCE   307 AA; 34203 MW; CB15B354 CRC32;

Qy   31 LSASL 35
Db 232 LSASL 236

Query Match   100.0%; Score 28; DB 3; Length 307;
Best Local Similarity   100.0%; Pred. No. 7.03e+02;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 14
ID   Q60458   PRELIMINARY;   PRT;   328 AA.
AC   Q60458;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   CATIONIC AMINO ACID TRANSPORTER-1 (FRAGMENT).
OS   CRICETULUS GRISEUS (CHINESE HAMSTER).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OVARY;
RA   WANG H., KLAMO E., KUHMANN S.E., KOZAK S., KAVANAUGH M.P., KABAT D.;
RL   SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U49797; I469943; -.
FT   NON_TER   1   1
FT   NON_TER   328   328
SQ   SEQUENCE   328 AA; 35208 MW; 0FD345C7 CRC32;

Qy   31 LSASL 35
Db 232 LSASL 236

Query Match   100.0%; Score 28; DB 11; Length 328;
Best Local Similarity   100.0%; Pred. No. 7.03e+02;
Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

RESULT 15
ID   032253   PRELIMINARY;   PRT;   340 AA.
AC   032253;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   YVBQ PROTEIN.
GN   YVBQ.
OS   BACILLUS SUBTILIS.

```
OC   PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RA   KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
RA   AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA   BORRISS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
RA   BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA   CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA   DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
RA   ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D., FRITZ C.,
RA   FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N., GHIM S.Y.,
RA   GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G., GUISEPPI G.,
RA   GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HENAUT A., HILBERT H.,
RA   HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L., JORIS B.,
RA   KARAMATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C., KOBAYASHI Y.,
RA   KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M., KURITA K., LAPIDUS A.,
RA   LARDINOIS S., LAUBER J., LAZAREVIC V., LEE S.M., LEVINE A., LIU H.,
RA   MASUDA S., MAUEL C., MEDIGUE C., MEDINA N., MELLADO R.P., MIZUNO M.,
RA   MOESTL D., NAKAI S., NOBACK M., NOONE D., O'REILLY M., OGAWA K.,
RA   OGIWARA A., OUDEGA B., PARK S.H., PARRO V., POHL T.M., PORTETELLE D.,
RA   PORWOLLIK S., PRESCOTT A.M., PRESECAN E., PUJIC P., PURNELLE B.,
RA   RAPOPORT G., REY M., REYNOLDS S., RIEGER M., RIVOLTA C., ROCHA E.,
RA   ROCHE B., ROSE M., SADAIE Y., SATO T., SCANLAN E., SCHLEICH S.,
RA   SCHROETER R., SCOFFONE F., SEKIGUCHI J., SEKOWSKA A., SEROR S.J.,
RA   SERROR P., SHIN B.S., SOLDO B., SOROKIN A., TACCONI E., TAKAGI T.,
RA   TAKAHASHI H., TAKEMARU K., TAKEUCHI M., TAMAKOSHI A., TANAKA T.,
RA   TERPSTRA P., TOGNONI A., TOSATO V., UCHIYAMA S., VANDENBOL M.,
RA   VANNIER F., VASSAROTTI A., VIARI A., WAMBUTT R., WEDLER E., WEDLER H.,
RA   WEITZENEGGER T., WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K.,
RA   YASUMOTO K., YATA K., YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E.,
RA   YOSHIKAWA H., DANCHIN A.;
RL   NATURE 390:249-256(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RA   KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
RL   SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; Z99121; E1186083; -.
SQ   SEQUENCE 340 AA; 37382 MW; 65C3FE2D CRC32;
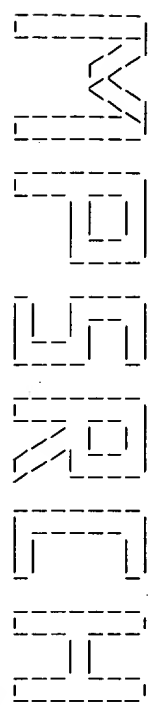```

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Query Match         100.0%;  Score 28;  DB 2;  Length 340;
Best Local Similarity 100.0%;  Pred. No. 7.03e+02;
Matches    5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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```
Db         40 LSASL 44
              |||||
           31 LSASL 35
```

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**************************************************************
      _____    ____    ____   ____    ____   _   _
     |  _  |  |  _ \  / ___| |  _ \  / ___| | | | |
     | |_| |  | |_) | \___ \ | |_) || |     | |_| |
     |  ___|  |  __/   ___) ||  _ < | |___  |  _  |
     |_|      |_|     |____/ |_| \_\ \____| |_| |_|   (TM)
**************************************************************
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

n on: Tue Apr 20 13:59:13 1999; MasPar time 2.77 Seconds
                 99.212 Million cell updates/sec

Tabular output not generated.

Title: >US-08-836-455-2
Description: (50-66) from US08836455.pep (2 of 3)
Perfect Score: 131
Sequence: 1 GINLHWLQEPDGTIKR 17

Scoring table: PAM 150
                 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: a ·geneseq32
                 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
                 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
                 14:part14 15:part15 16:part16 17:part17 18:part18
                 19:part19 20:part20 21:part21 22:part22 23:part23
                 24:part24 25:part25 26:part26 27:part27 28:part28
                 29:part29

Statistics: Mean 20.705; Variance 79.996; scale 0.259
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

### SUMMARIES

| Result No. | Score | % Match | Query Match Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 131 | 100.0 | 145 | 25 | W27119 | Murine monoclonal ant | 3.18e-05 |
| 2 | 110 | 84.0 | 107 | 25 | W27121 | Murine antibody light | 3.49e-03 |
| 3 | 110 | 84.0 | 107 | 4 | R21310 | Light chain of MiFc1 | 3.49e-03 |
| 4 | 110 | 84.0 | 109 | 25 | W18271 | PrP 37 light chain va | 3.49e-03 |
| 5 | 110 | 84.0 | 146 | 4 | P30251 | Sequence of the leade | 3.49e-03 |
| 6 | 105 | 80.2 | 243 | 18 | W00280 | 52OC9 anti-c-erbB-2 t | 1.05e-02 |
| 7 | 105 | 80.2 | 246 | 8 | R39569 | Sequence of 52OC9 sFv | 1.05e-02 |
| 8 | 105 | 73.3 | 534 | 8 | R39571 | Sequence of G-FIR | 7.41e-02 |
| 9 | 96 | 71.8 | 109 | 18 | R23030 | Sequence of G-FIR | 1.14e-01 |
| 10 | 94 | 71.8 | 90 | 16 | R80078 | Mouse derived light c | 1.14e-01 |
| 11 | 93 | 71.0 | 107 | 14 | R80078 | Light chain variable | 1.41e-01 |
| 12 | 93 | 71.0 | 107 | 14 | R79247 | Light chain variable | 1.41e-01 |
| 13 | 93 | 71.0 | 107 | 14 | R79250 | Light chain variable | 1.41e-01 |
| 14 | 93 | 71.0 | 128 | 24 | W22537 | Murine anti-human cla | 1.41e-01 |
| 15 | 91 | 69.5 | 109 | 4 | R21286 | Murine VL kappa group | 2.16e-01 |
| 16 | 88 | 67.2 | 109 | 25 | W18270 | PrP 28 light chain va | 4.09e-01 |
| 17 | 87 | 66.4 | 95 | 25 | W18269 | PrP 81 light chain va | 5.05e-01 |
| 18 | 85 | 64.9 | 124 | 9 | R47206 | Human/murine IL-1 ch1 | 7.70e-01 |
| 19 | 78 | 59.5 | 109 | 18 | R52040 | Light chain variable | 3.31e+00 |
| 20 | 78 | 59.5 | 127 | 6 | R28670 | pPM-k3 protein produc | 3.31e+00 |
| 21 | 78 | 59.5 | 273 | 10 | R52265 | Anti-influenza N10 sc | 3.31e+00 |
| 22 | 77 | 58.8 | 90 | 16 | R80079 | Mouse derived light c | 4.06e+00 |
| 23 | 76 | 58.0 | 107 | 6 | R30768 | Murine anti-CD3 MAb U | 4.99e+00 |
| 24 | 76 | 58.0 | 108 | 25 | W16620 | Anti-human FasL antib | 4.99e+00 |
| 25 | 76 | 58.0 | 108 | 21 | W00834 | Variable light chain | 4.99e+00 |
| 26 | 76 | 58.0 | 109 | 18 | W04177 | Variant variable ligh | 4.99e+00 |
| 27 | 76 | 58.0 | 126 | 2 | R52039 | Light chain variable | 4.99e+00 |
| 28 | 76 | 58.0 | 127 | 2 | R12237 | Light chain variable | 4.99e+00 |
| 29 | 76 | 58.0 | 127 | 23 | W11815 | Mouse MAb 1C11 L chai | 4.99e+00 |
| 30 | 76 | 58.0 | 127 | 2 | R12259 | Mouse anti-human Fas | 4.99e+00 |
| 31 | 76 | 58.0 | 128 | 6 | R29010 | p146-k3 protein produ | 4.99e+00 |
| 32 | 76 | 58.0 | 128 | 20 | W06215 | MAb ME4 light chain v | 4.99e+00 |
| 33 | 76 | 58.0 | 128 | 5 | R09426 | ME4 Light Chain V Reg | 4.99e+00 |
| 34 | 76 | 58.0 | 128 | 10 | R30776 | KM641 H chain variabl | 4.99e+00 |
| 35 | 76 | 58.0 | 128 | 7 | R53340 | Rat immunoglobulin L | 4.99e+00 |
| 36 | 76 | 58.0 | 131 | 14 | R33257 | MAb VL17E6 light chai | 4.99e+00 |
| 37 | 76 | 57.3 | 302 | 10 | R84553 | MAb SCH94.03 light ch | 4.99e+00 |
| 38 | 75 | 57.3 | 107 | 29 | R60206 | Bispecific CD3-L6tvIg | 6.12e+00 |
| 39 | 75 | 58.0 | 107 | 2 | W44122 | Light (kappa) chain v | 6.12e+00 |
| 40 | 73 | 55.7 | 214 | 20 | W00373 | H52L6-158 murine anti | 9.19e+00 |
| 41 | 73 | 55.7 | 214 | 26 | R99003 | Anti-CD18 chimeric an | 9.19e+00 |
| 42 | 72 | 55.0 | 127 | 20 | W99265 | Anti-CD18 light chai | 1.12e+01 |
| 43 | 72 | 54.2 | 127 | 8 | R39265 | Anti-CD4 antibody MT | 1.38e+01 |
| 44 | 71 | 54.2 | 209 | 26 | R64204 | Mouse C4G1 Ig light-c | 1.38e+01 |
| 45 | 70 | 53.4 | 209 | 26 | R64204 | Monoclonal antibody 1 | 1.68e+01 |
|  | 66 | 50.4 | 108 | 4 | R21292 | Murine VL kappa group | 3.72e+01 |

### ALIGNMENTS

```
RESULT 1
     W27119 standard; Protein; 145 AA.

ID   W27119 standard; Protein; 145 AA.
AC   W27119;
DT   04-JAN-1998 (first entry)
DE   Murine monoclonal anti-idiotype antibody 11D10 VL region.
KW   Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
KW   human milk fat globule; HMFG; tumour; breast cancer; vaccine.
OS   Mus musculus.
FH   Key            Location/Qualifiers
FT   Peptide        1..20
FT                  /label= Sig_peptide
FT   Protein        21..145
FT                  /label= Mat_protein
FT   Region         21..43
FT                  /label= FR1
FT                  /note= "framework region 1"
FT   Region         44..54
FT                  /label= CDR1
FT                  /note= "complementarity determining region 1"
FT   Region         55..69
FT                  /label= FR2
FT                  /note= "framework region 2"
FT   Region         70..76
FT                  /label= CDR2
FT                  /note= "complementarity determining region 2"
FT   Region         77..108
FT                  /label= FR3
FT                  /note= "framework region 3"
FT   Region         109..117
FT                  /label= CDR3
FT                  /note= "complementarity determining region 3"
FT   Region         118..127
FT                  /label= FR4
FT                  /note= "framework region 4"
PN   W09722699-A2.
PD   26-JUN-1997.
PF   19-DEC-1996; U20757.
PR   13-DEC-1996; US-575762.
PR   20-DEC-1995; US-575762.
PR   26-JAN-1996; US-591965.
PA   (KENT ) UNIV KENTUCKY.
PI   Chatterjee M, Chatterjee SK, Foon KA;
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DR   WPI; 97-341690/31.
DR   N-PSDB; T85149.
PT   Monoclonal anti-idiotype antibody 11D10 - elicits immune response
PT   against human milk fat globule disease associated tumours,
PS   especially breast cancer
PT   Claim 9; Page 94; 130pp; English.
CC   This polypeptide sequence comprises the light chain variable region
CC   (VL) of monoclonal anti-idiotype antibody 11D10 produced by
CC   hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
CC   naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype
CC   response. It elicits an immune response against a specific epitope
CC   of a high mol.wt. mucin of human milk fat globule (HMFG). It
CC   induces an immunological response to HMFG in mice, rabbits, monkeys
CC   and patients with advanced HMFG-associated tumours. Pharmaceutical
CC   compositions and vaccines comprising 11D10, 11D10 polypeptides
CC   and/or 11D10 polynucleotides (see also T85149-50) are claimed.
CC   Also claimed are diagnostic kits and methods of using 11D10, 11D10
CC   polypeptides and/or 11D10 polynucleotides, including methods of
CC   treating HMFG-associated tumours. 11D10 is also used in a claimed
CC   method of palliating HMFG-associated disease and in claimed kits to
CC   detect or quantify anti-HMFG antibody.
SQ   Sequence 145 AA;

Query Match             100.0%;  Score 131;  DB 25;  Length 145;
Best Local Similarity   100.0%;  Pred. No. 3.18e-05;
Matches    17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db         50  ginlhwlqqepdgtikr 66
               |||||||||||||||||
Qy         50  GINLHWLQQEPDGTIKR 66


RESULT   2
ID   W27121 standard; Protein; 107 AA.
AC   W27121;
DT   04-JAN-1998  (first entry)
DE   Murine antibody light chain variable region consensus.
KW   Monoclonal antibody light chain; anti-idiotype antibody; mucin;
KW   human milk fat globule; HMFG; tumour; breast cancer; vaccine.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   Region          24..34
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          50..56
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          88..96
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
PN   WO9722699-A2.
PD   26-JUN-1997.
PF   19-DEC-1996; US-575762.
PR   13-DEC-1996; US-575762.
PR   20-DEC-1995; US-575762.
PR   26-JAN-1996; US-591965.
PA   (KENT ) UNIV KENTUCKY.
PI   Chatterjee M, Chatterjee SK, Foon KA;
DR   WPI; 97-341690/31
PT   Monoclonal anti-idiotype antibody 11D10 - elicits immune response
PT   against human milk fat globule disease associated tumours,
PS   especially breast cancer
PT   Example 2; Fig 26C; 130pp; English.
CC   This polypeptide sequence comprises a consensus sequence of murine
CC   light chain variable regions (VL) selected on the basis of identity
CC   to the VL region (see W27119) of monoclonal anti-idiotype antibody
CC   11D10. The sequences were obtained from a GenBank database
CC   search. A VH consensus (W27122) was also produced. 11D10 has at
CC   least 18 departures from the consensus sequences (7 in the light
CC   chain and 11 in the heavy chain). 8 Occur within CDRs and 10
CC   outside CDRs. 11D10 polypeptides and polynucleotides can be
CC   used in vaccines and pharmaceutical compositions for the treatment
CC   of human milk fat globule-associated diseases such as breast
CC   cancer.
SQ   Sequence 107 AA;

Query Match              84.0%;  Score 110;  DB 25;  Length 107;
Best Local Similarity    82.4%;  Pred. No. 3.49e-03;
Matches    14;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Db         30  gsslnwlqqepdgtikr 46
               |:|||||||||||||||
Qy         50  GINLHWLQQEPDGTIKR 66


RESULT   3
ID   R21310 standard; Protein; 108 AA.
AC   R21310;
DT   21-MAY-1992  (first entry)
DE   Light chain of Mif clone.
KW   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW   plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW   specific binding pairs; replicable genetic display package.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   region          25..34
FT                   /label= CDR1
FT   region          50..56
FT                   /label= CDR2
FT   region          89..96
FT                   /label= CDR3
PN   WO9201047-A.
PD   23-JAN-1992.
PF   10-JUL-1991;  G01134.
PR   10-JUL-1990;  GB-015198.
PR   19-OCT-1990;  GB-0228645.
PR   12-NOV-1990;  GB-024503.
PR   06-MAR-1991;  GB-004744.
PR   15-MAY-1991;  GB-010549.
PA   (CAMB-) CAMBRIDGE ANTIBODY.
PA   (MEDI-) MED RES COUNCIL.
PI   McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI   Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI   Winter GP, Bonnert TP;
DR   WPI; 92-056862/07.
PT   Producing members of specific binding pairs - by expression in
PT   recombinant host cells with a secreting replicable genetic
PT   display package.
PS   Example 46; Fig 52; 109pp; English.
CC   The sequence is the light chain of clone MIF encoding an scFv frag-
CC   ment specific for both hen and turkey egg lysozyme (HEL and TEL).
CC   The DNA encoding the chain was amplified from a cDNA library prepd.
CC   from the spleen of an unimmunised mouse. The corresponding heavy
CC   chain was also amplified from an existing construct, PSW1-VHD1.3
CC   (Ward et al, 1989). The two fragments were assembled via a linker
CC   to prepare an scFv construct which was ligated into the fdCAT2
CC   vector for expression on the surface of fd bacteriophage. In this
CC   way, the VL domain was replaced by a library of VL domains to allow
CC   for selection of a broader range of antibody specificities. Several
CC   clones were isolated which bound to TEL (the parent antibody D1.3
CC   binds exclusively to HEL). The sequences of the light chains of
CC   two of these clones, MFl and M21 are given in R21310 and R21311
CC   respectively. The D1.3 light chain is given in R21309.
CC   See also R21260-307, 309-312, R22450, R22565, R22567-81.
SQ   Sequence 108 AA;

Query Match              84.0%;  Score 110;  DB 4;  Length 108;
Best Local Similarity    82.4%;  Pred. No. 3.49e-03;
Matches    14;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Db         30  gsslnwlqqepdgtikr 46
               |:|||||||||||||||
Qy         50  GINLHWLQQEPDGTIKR 66


RESULT   4
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ID   W18271 standard; peptide; 109 AA.
AC   W18271;
DT   09-JAN-1998 (first entry)
DE   PrP 37 light chain variable region.
KW   Prion protein; PrP; heavy chain variable region; antibody; scrapie;
KW   light chain variable region; PrP-Sc; pathogen; fatal familial insomnia;
KW   central nervous system spongiform encephalopathy disease; human; therapy;
KW   transmissible neurodegenerative disease; feline spongiform encephalopathy;
KW   bovine spongiform encephalopathy; Creutzfeldt-Jakob Disease;
KW   Gerstmann-Strassler-Scheinker Disease.
OS   Mus musculus.
FH   Key   Location/Qualifiers
FT   Region   1..23
FT   /note= "framework region 1"
FT   Region   24..34
FT   /note= "complementarity determining region 1"
FT   Region   35..49
FT   /note= "framework region 2"
FT   Region   50..56
FT   /note= "complementarity determining region 2"
FT   Region   57..88
FT   /note= "framework region 3"
FT   Region   89..97
FT   /note= "complementarity determining region 3"
FT   Region   98..109
FT   /note= "framework region 4"
PN   WO9710505-A1.
PD   20-MAR-1997.
PF   13-SEP-1996; U14840.
PR   14-SEP-1995; US-528104.
PA   (REGC) UNIV CALIFORNIA.
PI   Burton DR, Prusiner SB, Williamson RA;
PT   New antibodies to the scrapie isoform of prion protein - used for
PT   detection of infectious prion proteins or for treating disease such
PT   as BSE, CJD or scrapie
PS   Example 9; Fig 6; 99pp; English.
DR   WPI; 97-202357/18.
CC   W18266-W18285 represent portions of the antibodies of the invention. The
CC   antibodies of the invention are able to bind the scrapie isoform of prion
CC   protein PrP-Sc in situ. Prions are infectious pathogens that cause
CC   central nervous system spongiform encephalopathies in humans and animals.
CC   The scrapie isoform of the prion protein (PrP-Sc) is necessary for both
CC   the transmission and pathogenesis of the transmissible neurodegenerative
CC   diseases of animals and humans. The antibodies can be used in a method of
CC   the invention for detecting human PrP-Sc in a source. The antibodies
CC   specifically bind to prion proteins associated with disease and do not
CC   bind to denatured PrP proteins not associated with disease. They can bind
CC   to prion proteins of a specific species of mammals. They can also have
CC   the ability to neutralise infectious prions. The antibodies can be used
CC   for screening for the presence of prions in products such as
CC   pharmaceuticals, food or cosmetics. They can also be used for prion
CC   neutralisation to purify products, for extraction of prion proteins or
CC   for therapy, for diseases such as bovine spongiform encephalopathy,
CC   Creutzfeldt-Jakob Disease, fatal familial insomnia or
CC   Gerstmann-Strassler-Scheinker Disease, scrapie or feline spongiform
CC   encephalopathies.
SO   Sequence 109 AA;

Query Match   84.0%; Score 110; DB 25; Length 109;
Best Local Similarity   82.4%;
Matches   14; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   30 gsslnwlqqepdgtikr 46
              |:|:||||||||||||||
Db   50 GINLHWLQQEPDGTIKR 66

RESULT 5
ID   P30251 standard; peptide; 146 AA.
AC   P30251;
DT   25-MAY-1992 (first entry)
DE   Sequence of the leader, variable region and first 16 AAs of
DE   the constant region of the kappa-chain (light chain) of MOPC41.
KW   Diagnosis; therapy; immunoglobulin.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   region   1..22
FT   /label= leader
FT   region   23..130
FT   /label= variable
FT   region   131..146
FT   /label= constant
PN   EP-88994-A.
PD   21-SEP-1983.
PF   10-MAR-1983; 001655.
PR   15-MAR-1982; US-358414.
PR   05-DEC-1983; US-558551.
PA   (SCHE) SCHERING CORP.
PA   (DNAX) DNAX RES INST.
PI   Moore KW, Zaffaroni A;
DR   WPI; 83-772290/39.
DR   N-PSDB; N30165.
PT   Transformed expression vectors or plasmid(s) - with double
PT   stranded DNA sequence coding only for desired part of polypeptide
PT   chain
PS   Example; Page 40-41; 68pp; English.
CC   The pref. vector or plasmid of the invention has a double-stranded
CC   DNA seq. coding for a variable region of a light or heavy chain of
CC   IgG, or for a variable region of a light or heavy chain of an
CC   immunoglobulin specific for an enzyme or surface protein. The
CC   sequence esp. codes for a variable region of a light chain having 95-
CC   115 AAs or for a variable region of a heavy chain having 110-125 AAs
CC   esp. including the D region of the heavy chain.
SO   Sequence 146 AA;

Query Match   84.0%; Score 110; DB 4; Length 146;
Best Local Similarity   82.4%;
Matches   14; Conservative   2; Mismatches   1; Indels   0; Gaps   0;

Qy   52 gsslnwlqqepdgtikr 68
              |:|:||||||||||||||
Db   50 GINLHWLQQEPDGTIKR 66

RESULT 6
ID   W02280 standard; Protein; 243 AA.
AC   W02280;
DT   29-OCT-1996 (first entry)
DE   520C9 anti-c-erbB-2 two single chain Fv construct.
KW   520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sFv;
KW   construct; polypeptide linker; C-terminal amino acid sequence;
KW   in vivo imaging; drug targeting experiment; homodimer;
KW   increased; binding avidity; tissue retention time.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FT   peptide   118..133
FT   /label= linker
PN   US5534254-A.
PD   09-JUL-1996.
PF   06-FEB-1992; 831967.
PF   06-FEB-1992; US-831967.
PR   07-OCT-1993; US-133804.
PA   (CHIR) CHIRON CORP.
PA   (CREA-) CREATIVE BIOMOLECULES INC.
PI   Houston LL, Huston JS, Oppermann H, Ring DB;
DR   WPI; 96-333194/33.
DR   N-PSDB; T36880.
PT   Compsns. contg. antigen-targeting antibody fragment constructs -
PT   comprising dimer of single-chain Fv
PS   Example 1; Columns 33-36; 30pp; English.
CC   Variable heavy (VH) and variable light (VL) genes were cloned from
CC   a 520C9 hybridoma cDNA library, using probes directed toward the
CC   antibody constant and joining regions. A two single chain Fv (sFv)
CC   gene was constructed by connecting the VH and VL genes with a
CC   Ser rich polypeptide linker. The resulting 520C9 two sFv gene,
CC   which encodes the present sequence, was inserted into an expression

CC vector, transformed into E. coli, and protein expression induced by
CC the addn. of IPTG to the culture medium.
CC A compsn. comprising a carrier and the 2 sFv protein prod. can be
CC used for in vivo imaging, and drug targeting experiments. The
CC 2 sFv protein prod. is a homodimer, in which both fragments target
CC the same antigen, therefore giving greater binding avidity and
CC longer tissue retention times, compared to individual sFv protein
CC prod. fragments.
SQ Sequence 243 AA;

Qy 163 gnsltwlqqepdgtikr 179
        |:||||||||||||||||
Db   50 GINLHWLQQEPDGTIKR 66

Query Match   80.2%; Score 105; DB 18; Length 243;
Best Local Similarity   82.4%; Pred. No. 1.05e-02;
Matches   14; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

RESULT 7
ID R39569 standard; Protein; 246 AA.
AC R39569;
DT 07-FEB-1994 (first entry)
DE Sequence of 520C9 sFv protein.
KW biosynthetic single polypeptide chain binding site; ss.
OS Synthetic.
PN WO9316185-A.
PD 19-AUG-1993.
PF 05-FEB-1993; U01055.
PR 06-FEB-1992; US-831967.
PA (CETU) CETUS ONCOLOGY CORP.
PA (CREA-) CREATIVE BIOMOLECULES INC.
PI Houston LL, Huston JS, Oppermann H, Ring DB;
DR WPI; 93-272889/34.
DR N-PSDB; Q46084.
PT New single chain Fv polypeptide binding to C-erbB-2 tumour
PT antigen - for imaging or treating breast or ovarian cancer etc.
PS Claim 4; Pages 60-61; 87pp; English.
CC c-erbB-2 refers to a protein antigen expressed on the surface of
CC tumour cells, such as breast and ovarian tumour cells, which is an
CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
CC pt. of about 5.3 (see Q46083, R39568). A single chain Fv (sFv)
CC is a covalently linked VH- and VL-heterodimer which is expressed from
CC a gene fusion including VH- and VL- encoding genes connected by
CC a peptide-encoding linker. Such linker sequences are set forth in
CC AA residues 116-135 in R39569, which includes part of the 16 AA
CC linker sequences in R39572. Using Q46084 for the 520C9 monoclonal
CC antibody, a single chain polypeptide can be produced having a
CC binding affinity for a c-erbB-2 related antigen. 'x' in R39569
CC refers to the location of a stop codon in Q46084.
SQ Sequence 246 AA;

Qy 163 gnsltwlqqepdgtikr 179
        |:||||||||||||||||
Db   50 GINLHWLQQEPDGTIKR 66

Query Match   80.2%; Score 105; DB 8; Length 246;
Best Local Similarity   82.4%; Pred. No. 1.05e-02;
Matches'   14; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

RESULT 8
ID R39571 standard; Protein; 534 AA.
AC R39571;
DT 07-FEB-1994 (first entry)
DE Sequence of G-FIT.
KW Tumour antigen; c-erbB-2; G-FIT.
OS Synthetic.
PN WO9316185-A.
PD 19-AUG-1993.
PF 05-FEB-1993; U01055.
PR 06-FEB-1992; US-831967.

PA (CETU) CETUS ONCOLOGY CORP.
PA (CREA-) CREATIVE BIOMOLECULES INC.
PI Houston LL, Huston JS, Oppermann H, Ring DB;
DR WPI; 93-272889/34.
DR N-PSDB; Q46086.
PT New single chain Fv polypeptide binding to C-erbB-2 tumour
PT antigen - for imaging or treating breast or ovarian cancer etc.
PS Example; pages 65-68; 87pp; English.
CC c-erbB-2 refers to a protein antigen expressed on the surface of
CC tumour cells, such as breast and ovarian tumour cells, which is an
CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
CC pt. of about 5.3 (see Q46083, R39568).
SQ Sequence 534 AA;

Db 454 gnsltwlsqepdgtikr 470
        |:||||||||||||||||
Qy   50 GINLHWLQQEPDGTIKR 66

Query Match   73.3%; Score 96; DB 8; Length 534;
Best Local Similarity   76.5%; Pred. No. 7.41e-02;
Matches   13; Conservative   1; Mismatches   3; Indels   0; Gaps   0;

RESULT 9
ID R52030 standard; Protein; 109 AA.
AC R52030;
DT 26-SEP-1996 (first entry).
DE Light chain variable region of murine antibody glb2.
KW antibody; humanised; murine; human; heavy chain; light; variable;
KW framework region; complementarity determining region; reshaping;
OS modelling; surface residue; modify.
OS Mus sp.
FH Key   Location/Qualifiers
FT region   1..23
FT   /label= framework_region_1
FT region   24..34
FT   /note= "FR 1"
FT region   35..49
FT   /note= "CDR 1"
FT   /label= complementarity_determining_region_1
FT region   50..56
FT   /label= FR_2
FT region   57..88
FT   /label= CDR_2
FT region   89..97
FT   /label= FR_3
FT region   98..109
FT   /label= CDR_3
FT region
FT   /label= FR_4

DR WPI; 94-120230/15.
DR Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
PA (IMMU-) IMMUNOGEN INC.
PA (PEDE/) PEDERSEN J T.
PR 09-SEP-1992; US-942245.
PD 13-APR-1994.
PN EP-592106-A1.
DR 07-SEP-1993; 307051.
DR 13-APR-1994.
PT Method of resurfacing of rodent antibodies to produce humanised
PT antibody forms - for producing non-human antibodies with improved
PT therapeutic efficiency by presenting human surface on V-region
PS Example 1; Fig 3A; 230pp; English.
CC The present sequence is that of the light chain variable (LC VR) region
CC of murine antibody glb2. This sequence was aligned with 11 other known
CC antibody LC VRs and a set of framework positions of surface exposed amino
CC acid residues was determined. This information can be used in a method to
CC determine how to modify a rodent antibody or fragment by resurfacing in
CC order to produce a humanised rodent antibody. Residues (determined from
CC alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86,
CC 87, 111, 115, 116 and 117 are accessible residues. None of the entire
CC combinations of surface residues in the murine sequences were found in
CC the human sequences and vice versa. However the residues in individual
CC positions appear to be conserved.
SQ Sequence 109 AA;

Qy   50 GINLHWLQQEPDGTIKR 66

Query Match   71.8%;   Score 94;   DB 18;   Length 109;
Best Local Similarity 85.7%;   Pred. No. 1.14e-01;
Matches   12;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

Db   33 lswlgqkpdgtikr 46
         ||||| ||||||
Qy   53 LHWLQQEPDGTIKR 66

RESULT   10
ID   R80078 standard; Protein; 90 AA.
AC   R80078;
DT   22-MAY-1996 (first entry)
DE   Mouse derived light chain RT3 phage antibody pattern A.
KW   Light chain; RT3; murine; catalytic antibody; bacteriophage;
KW   pattern A.
OS   Mus musculus.
FH   Key   Location/Qualifiers
FT   region   1..15
FT   /note= "framework region 1"
FT   region   16..26
FT   /note= "complementarity determining region 1"
FT   region   27..40
FT   /note= "framework region 2"
FT   region   41..47
FT   /note= "complementarity determining region 2"
FT   region   48..78
FT   /note= "framework region 3"
FT   region   79..88
FT   /note= "complementarity determining region 3"
FT   region   89..90
FT   /note= "framework region 4"
FT   /note= "N-terminal fragment"
PN   WO9527045-A1.
PD   12-OCT-1995.
PD   30-MAR-1994; WO3420.
PR   30-MAR-1994; WO-003420.
PA   (IGEN-) IGEN INC.
PI   Chiswell D, Darsley MJ, Fitzgerald K, Kenten JH;
PI   Martin MT, McCafferty J, Smith RG, Titmas RC, Williams RO;
DR   WPI; 95-356524/46.
DR   N-PSDB; T04625.
PT   Production of catalytic antibodies displayed on phage - by
PT   generating a gene library of antibody-derived domains and expressing
PT   it in phage vectors
PS   Disclosure; Fig 9; 133pp; English.
CC   T04625 encodes R80078 mouse derived light chain RT3 phage antibody.
CC   The DNA was used in the prepn. of catalytic antibody (CA) producing
CC   bacteriophage. The CAs can be used to activate/deactivate a
CC   biological function in an animal by enhancing the rate of cleavage,
CC   or formation of a specific bond within a mol. in vivo.
SQ   Sequence   90 AA;

Query Match   71.0%;   Score 93;   DB 16;   Length 90;
Best Local Similarity 76.5%;   Pred. No. 1.41e-01;
Matches   13;   Conservative   2;   Mismatches   1;   Indels   1;   Gaps   1;

Db   22 gsslnwlgqep-gtikr 37
         |:|:||||||| ||||
Qy   50 GINLHWLQQEPDGTIKR 66

RESULT   11
ID   R79247 standard; Protein; 107 AA.
AC   R79247;
DT   21-DEC-1995 (first entry)
DE   Light chain variable region for monoclonal antibody 1F10.
KW   Monoclonal antibody; heavy metal; mercury; variable region;
KW   light chain.
OS   Synthetic.
PN   WO9520607-A.
PD   03-AUG-1995.

PF   27-JAN-1995; U01199.
PR   27-JAN-1994; US-187407.
PA   (BION-) BIONEBRASKA INC.
PI   Lopez O, Wagner FW, Wylie DE;
WPI; 95-275415/36.
DR   N-PSDB; Q97504.
PT   New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT   monoclonal antibodies, used for detecting, removing, adding or
PI   neutralising heavy metals
PS   Claim 23; Page 62; 106pp; English.
CC   Hybridoma antibodies have been produced with the spleen cells of
CC   BALB/c mouse that had received multiple injections of mercuric ions
CC   reacted with glutathione to produce a mercuric ion coordinate
CC   covalent compound which was covalently bound to keyhole limpet
CC   hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC   5B6 and 3E8) were producing MAbs that were strongly positive
CC   against glutathione-mercuric ions but negative against glutathione
CC   without mercuric ions. RNA was isolated from hybridoma cells with
CC   guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC   by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC   were complementary to the 5' end of the CH1 domain of the heavy
CC   chain expressed by the hybridoma of interest, or to the 5' end of
CC   the C kappa domain. Some of the primers used for cDNA synthesis are
CC   shown in Q97511-Q97518. The primer used for cDNA synthesis of the
CC   variable region of a particular antibody polypeptide was also used
CC   for PCR amplification of that variable region, in conjunction with
CC   an appropriate v-region primer. In addition, the VH primer Q97518
CC   was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC   of the PCR amplified nucleotides were determined. These are given
CC   in Q97498-Q97510 and the deduced AA sequences in R79241-R79250 &
CC   R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC   and in the claims are different from the descriptions in the
CC   sequence listings. The descriptions in the sequence listings are
CC   used here.
SQ   Sequence   107 AA;

Query Match   71.0%;   Score 93;   DB 14;   Length 107;
Best Local Similarity 70.6%;   Pred. No. 1.41e-01;
Matches   12;   Conservative   2;   Mismatches   3;   Indels   0;   Gaps   0;

Db   30 gsslnwlglkpdgtikr 46
         |:|:||| |||||||
Qy   50 GINLHWLQQEPDGTIKR 66

RESULT   12
ID   R78972 standard; Protein; 107 AA.
AC   R78972;
DT   21-DEC-1995 (first entry)
DE   Light chain variable region for monoclonal antibody 5B6.
KW   Monoclonal antibody; heavy metal; mercury; variable region;
KW   light chain.
OS   Synthetic.
PN   WO9520607-A.
PD   03-AUG-1995.
PF   27-JAN-1995; U01199.
PR   27-JAN-1994; US-187407.
PA   (BION-) BIONEBRASKA INC.
PI   Lopez O, Wagner FW, Wylie DE;
WPI; 95-275415/36.
DR   N-PSDB; Q97510.
PT   New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT   monoclonal antibodies, used for detecting, removing, adding or
PT   neutralising heavy metals
PS   Claim 23; Page 70; 106pp; English.
CC   Hybridoma antibodies have been produced with the spleen cells of
CC   BALB/c mouse that had received multiple injections of mercuric ions
CC   reacted with glutathione to produce a mercuric ion coordinate
CC   covalent compound which was covalently bound to keyhole limpet
CC   hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC   5B6 and 3E8) were producing MAbs that were strongly positive
CC   against glutathione-mercuric ions but negative against glutathione
CC   without mercuric ions. RNA was isolated from hybridoma cells with

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CC   guanidine isothiocyanate. First strand-cDNA synthesis was catalysed
CC   by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC   were complementary to the 5' end of the CH1 domain of the heavy
CC   chain expressed by the hybridoma of interest, or to the 5' end of
CC   the C kappa domain. Some of the primers used for cDNA synthesis of
CC   the variable region of a particular antibody polypeptide was also used
CC   for PCR amplification of that variable region, in conjunction with
CC   an appropriate V-region primer. In addition, the VH primer Q97518
CC   was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC   shown in Q97511-Q97518. The primer used for cDNA synthesis of the
CC   variable region of a particular antibody polypeptide was also used
CC   for PCR amplification of that variable region. In addition, the VH primer Q97518
CC   was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC   of the PCR amplified nucleotides were determined. These are given
CC   in Q97498-Q97510 and the deduced AA sequences in R79241-R79250 &
CC   R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC   and in the claims are different from the descriptions in the
CC   sequence listings. The descriptions in the sequence listings are
CC   used here.
SQ   Sequence 107 AA;

Qy  Query Match    71.0%;  Score 93;  DB 14;  Length 107;
    Best Local Similarity  70.6%;  Pred. No. 1.41e-01;
    Matches   12;  Conservative   2;  Mismatches   3;  Indels   0;  Gaps   0;

Db       30 gsslnwlqlkpdgtikr 46
            |:l:||||||||||||||
Qy       50 GINLHWLQQEPDGTIKR 66

RESULT 13
ID   R79250 standard; Protein; 107 AA.
AC   R79250;
DT   21-DEC-1995 (first entry)
DE   Light chain variable region for monoclonal antibody 5G4.
KW   Monoclonal antibody; heavy metal; mercury; variable region;
KW   light chain.
OS   Synthetic.
PN   WO9520607-A.
PD   03-AUG-1995.
PF   27-JAN-1995; U01199.
PR   27-JAN-1994; US-187407.
PA   (BION-) BIONEBRASKA INC.
PI   Lopez O, Wagner FW, Wylie DE;
DR   WPI; 95-275415/36.
DR   N-PSDB; Q97507.
CC   New polypeptide(s) which bind heavy metals, esp. mercury - derived from
CC   monoclonal antibodies, used for detecting, removing, adding or
CC   neutralising heavy metals
CC   Claim 23; Page 66; 106pp; English.
CC   Hybridoma antibodies have been produced with the spleen cells of
CC   BALB/c mouse that had received multiple injections of mercuric ions
CC   reacted with glutathione to produce a mercuric ion coordinate
CC   covalent compound which was covalently bound to keyhole limpet
CC   hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC   5B6 and 3E8) were producing MAbs that were strongly positive
CC   against glutathione-mercuric ions but negative against glutathione
CC   without mercuric ions. RNA was isolated from hybridoma cells with
CC   guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC   by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC   were complementary to the 5' end of the CH1 domain of the heavy
CC   chain expressed by the hybridoma of interest, or to the 5' end of
CC   the C kappa domain. Some of the primers used for cDNA synthesis of the
CC   variable region of a particular antibody polypeptide was also used
CC   for PCR amplification of that variable region, in conjunction with
CC   an appropriate V-region primer. In addition, the VH primer Q97518
CC   was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC   shown in Q97511-Q97518. The primer used for cDNA synthesis of the
CC   variable region of a particular antibody polypeptide was also used
CC   for PCR amplification of that variable region. In addition, the VH primer Q97518
CC   was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC   of the PCR amplified nucleotides were determined. These are given
CC   in Q97498-Q97510 and the deduced AA sequences in R79241-R79250 &
CC   R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC   and in the claims are different from the descriptions in the
CC   sequence listings. The descriptions in the sequence listings are
CC   used here.
SQ   Sequence 107 AA;


Qy  Query Match    71.0%;  Score 93;  DB 14;  Length 107;
    Best Local Similarity  70.6%;  Pred. No. 1.41e-01;
    Matches   12;  Conservative   2;  Mismatches   3;  Indels   0;  Gaps   0;

Db       30 gsslnwlqlkpdgtikr 46
            |:l:||||||||||||||
Qy       50 GINLHWLQQEPDGTIKR 66

RESULT 14
ID   W22537 standard; Protein; 129 AA.
AC   W22537;
DT   03-NOV-1997 (first entry)
DE   Murine anti-human class II monoclonal antibody 44H104 VL chain.
DE   Antibody; light chain; variable region; hybridoma cell line 44H104;
KW   immune response; enhance; stimulate; vaccine; immunodiagnosis;
KW   antigen delivery.
OS   Mus musculus.
PN   WO9640941-A1.
PD   19-DEC-1996.
PF   07-JUN-1996; CA0400.
PR   07-JUN-1995; US-483576.
PA   (CONN-) CONNAUGHT LAB LTD.
PI   Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH;
DR   N-PSDB; T77851.
DR   WPI; 97-077271/07.
PT   Recombinant conjugate antibody mol., modified for delivering an
PT   antigen - elicits enhanced immune response without the use of
PT   adjuvant to generate antibodies which are useful in vaccines or
PT   immuno:diagnosis
PS   Example 1; Fig 1A; 64pp; English.
CC   Novel recombinant conjugate antibody molecules comprise a monoclonal
CC   antibody specific for a surface structure of antigen presenting
CC   cells (APC), genetically modified to contain at least one antigen
CC   exclusively at one or more preselected sites. The conjugate is capable
CC   of delivering the antigen to APC and eliciting an immune response to
CC   the antigen. The new conjugates are useful as vaccines and are able
CC   to elicit an enhanced immune response without the use of an adjuvant.
CC   In a specific example, a conjugate was constructed using the murine
CC   anti-human class II monoclonal antibody secreted by hybridoma
CC   44H104. The peptide CLTB36 was chosen as antigen; it consists of
CC   a tandemly linked T and B cell epitope derived from HIV MN strain.
CC   The present sequence represents the light chain variable region
CC   from 44H104 which was used in the preparation of a conjugate with
CC   antigen CLTB36.
SQ   Sequence 129 AA;

Qy  Query Match    71.0%;  Score 93;  DB 24;  Length 129;
    Best Local Similarity  85.7%;  Pred. No. 1.41e-01;
    Matches   12;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Db       55 ltwlqqkpdgtikr 68
            | |||.|| ||||||
Qy       53 LHWLQQEPDGTIKR 66

RESULT 15
ID   R21286 standard; Protein; 108 AA.
AC   R21286;
DT   21-MAY-1992 (first entry)
DE   Murine VL kappa group V chain "a", specific for phox.
KW   Fd; bacteriophage; gene III; filamenous; phagemid; capsid; coat;
KW   pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW   specific binding pairs; replicable genetic display package.
OS   Synthetic.
FH   Key              Location/Qualifiers
FT   binding_site     24..34
FT                    /label= CDR3
FT                    /note= "D-X-G-X-X motif "
FT   binding_site     50..56
FT                    /label= CDR1
FT   binding_site     89..96
FT                    /label= CDR2
```

PN   WO9201047-A.
PD   23-JAN-1992.
PF   10-JUL-1991; G01134.
PF   10-JUL-1990; GB-015198.
PR   19-OCT-1990; GB-022845.
PR   12-NOV-1990; GB-024503.
PR   06-MAR-1991; GB-004744.
PR   15-MAY-1991; GB-010549.
PA   (CAMB-) CAMBRIDGE ANTIBODY.
PA   (MEDI-) MED RES COUNCIL.
PI   McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI   Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI   Winter GP, Bonnert TP;
DR   WPI; 92-056862/07.
PT   Producing members of specific binding pairs - by expression in
PT   recombinant host cells with a secreting replicable genetic
PT   display package.
PS   Example 21; Fig 24; 209pp; English.
CC   The VK sequence is one of seven (R21286-92) found to be expressed
CC   from a single chain Fv library from an immunised mouse. The libra-
CC   ry produces a diverse repertoire of antibody fragments specific for
CC   2-phenyl-5-oxazolone (phOx). It was prepd. using cDNA generated
CC   from mRNA from mice immunised with phOx coupled to chicken serum
CC   albumin. The VH and VL kappa sequences were separately amplified
CC   by PCR (see O23474-84) and ligated into fdCAT2 (see O23463) for ex-
CC   pression on the phage surface as fusions with gene III. The result-
CC   ing library of clones was diverse. Twenty three hapten binding
CC   clones were sequenced revealing eight different VH genes (A-H) (see
CC   R21264-71) in a variety of pairings with the seven different Vk
CC   genes (a-g). Of the twenty three clones sequenced, three were of
CC   type "a", and were "ox-like" genes.   (See Berek et al, Nature 316
CC   412-418, 1985).   They contain the DXGXX motif in CDR3, the central
CC   Gly of which is needed to create a cavity for phOx. Most of the
CC   clones were Vk-d combinations. The Kd of VH-B/Vk-d for phOx-GABA
CC   was 10 nM. Only two other combinations (of eleven tested) were
CC   found to have higher values. This suggests that phage bearing scFv
CC   fragments having weak affinities can be selected with antigen, pro-
CC   bably due to the avidity of the multiple antibody heads on the
CC   phage.
CC   See also R21260-307, 309-311; R22450, 565-581.
SQ   Sequence   108 AA;

Query Match   69.5%; Score 91; DB 4; Length 108;
Best Local Similarity   78.6%; Pred. No. 2.16e-01;
Matches   11; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

Db   33 lswlqqkpdgsikr 46
                | |||| ||:|||
Qy   53 LHWLQQEPDGTIKR 66

Search completed: Tue Apr 20 13:59:29 1999
Job time : 16 secs.

MPSRCH (TM)

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 20 13:58:42 1999; MasPar time 3.59 Seconds
                                          177.483 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-836-455-2
                   (50-66) from US08364655.pep (2 of 3)
Perfect Score: 131
Sequence: 1 GINLHWLQQEPDGTIKR 17

Scoring table: PAM 150
                   Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0%
                   Listing first 45 summaries

Database: pir58
                   1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 28.231; Variance 51.804; scale 0.545

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match Length	DB	ID	Description	Pred. No.
1	110	84.0	88	2	PL0261	Ig kappa chain V regi	2.15e-07
2	110	84.0	106	2	PL0260	Ig kappa chain V regi	2.15e-07
3	110	84.0	106	2	PL0259	Ig kappa chain V regi	2.15e-07
4	110	84.0	130	2	KVMSM4	Ig kappa chain precur	2.15e-07
5	94	71.8	98	2	PH1062	Ig light chain V regi	1.45e-04
6	94	71.8	106	2	PL0262	Ig kappa chain V regi	1.45e-04
7	91	69.5	91	2	S17622	Ig kappa chain V regi	4.70e-04
8	91	69.5	108	4	B47271	nitrophenyl phosphona	4.70e-04
9	90	68.7	92	2	D28840	Ig kappa chain V regi	6.95e-04
10	90	68.7	101	2	D28840	Ig kappa chain V regi	6.95e-04
11	84	64.1	101	2	C28840	Ig kappa chain V regi	6.97e-03
12	84	64.1	93	2	S38564	Ig kappa chain V regi	6.97e-03
13	76	58.0	105	2	PH0087	Ig kappa chain V regi	1.35e-01
14	76	58.0	107	2	A48677	Ig kappa chain V-J re	1.35e-01
15	76	58.0	107	2	B48677	Ig kappa chain V-J re	1.35e-01
16	76	58.0	107	2	A28044	Ig kappa chain V regi	1.35e-01
17	76	58.0	107	2	B49026	Ig kappa chain V regi	1.35e-01
18	76	58.0	107	2	B28044	Ig kappa chain V regi	1.35e-01
19	76	58.0	107	2	C48677	Ig light chain V-J re	1.35e-01
20	76	58.0	107	2	D48677	Ig light chain V-J re	1.35e-01
21	76	58.0	107	2	S69901	Ig kappa chain (clone	1.35e-01
22	76	58.0	107	2	S99906	Ig kappa chain (clone	1.35e-01
23	76	58.0	108	2	B26405	Ig kappa chain V regi	1.35e-01
24	76	58.0	108	2	S69902	Ig kappa chain (clone	1.35e-01
25	76	58.0	108	1	KVMSAR	Ig kappa chain V regi	1.35e-01
26	76	58.0	108	2	S69903	Ig kappa chain (clone	1.35e-01
27	76	58.0	108	2	C26405	Ig kappa chain V regi	1.35e-01
28	76	58.0	108	2	S11124	Ig kappa chain V regi	1.35e-01
29	76	58.0	108	2	S69900	Ig kappa chain V regi	1.35e-01
30	76	58.0	108	2	S38862	Ig kappa chain precur	1.35e-01
31	76	58.0	108	2	PL0282	Ig kappa chain V regi	1.35e-01
32	76	58.0	109	2	PH0888	Ig kappa chain (clone	1.35e-01
33	76	58.0	128	2	A26406	Ig kappa chain V-J re	1.35e-01
34	76	58.0	111	2	B72266	Ig kappa chain V regi	1.35e-01
35	76	58.0	111	2	G38740	Ig kappa chain V regi	1.35e-01
36	76	58.0	111	2	A38740	Ig kappa chain V regi	1.35e-01
37	76	58.0	111	2	E38740	Ig kappa chain V regi	1.35e-01
38	76	58.0	115	2	I38740	Ig kappa chain V regi	1.35e-01
39	76	58.0	115	2	JL0080	Ig kappa chain precur	1.94e-01
40	76	58.0	122	2	A29380	Ig kappa chain precur	1.35e-01
41	76	58.0	126	2	A34904	Ig kappa chain V regi	1.35e-01
42	76	58.0	128	2	A26406	Ig kappa chain V-J re	1.35e-01
43	77.3	57.3	107	2	S32188	Ig kappa chain V regi	1.94e-01
44	77.3	57.3	108	2	B30551	Ig kappa chain V regi	1.94e-01
45	75	57.3	129	2	D32513	Ig kappa chain precur	1.94e-01

ALIGNMENTS

RESULT 1
ENTRY   PL0261   #type fragment
TITLE   Ig kappa chain V region (anti-DNA, DP15VK) - mouse mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
              09-May-1997
ACCESSIONS   PL0261
REFERENCE   PL0261
              Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
              D.; Marshak-Rothstein, A.; Weigert, M.
              #journal   J. Exp. Med. (1990) 171:265-297
              #title   Anti-DNA antibodies from autoimmune mice arise by clonal
              expansion and somatic mutation.
              #cross-references MUID:90111618
              #accession PL0261
              ##molecule_type mRNA
              ##residues   1-88 ##label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
FEATURE
              1-5   #region framework 1\
              6-16   #region complementarity-determining 1\
              17-31   #region framework 2\
              32-38   #region complementarity-determining 2\
              39-70   #region framework 3\
              71-79   #region complementarity-determining 3\
              80-88   #region framework 4
SUMMARY   #length 88   #checksum 7092

Query Match   84.0%;   Score 110; DB 2; Length 88;
Best Local Similarity   82.4%;   Pred. No. 2.15e-07;
Matches 14;   Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy   50 GINLHWLQQEPDGTIKR 66
              :|:||||||||||||||
Db   12 GSSLNWLQQEPDGTIKR 28

RESULT 2
ENTRY   PL0260   #type fragment
TITLE   Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
              16-Aug-1996
ACCESSIONS   PL0260
REFERENCE   PL0260
              PL0231
              Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,

RESULT 3

ENTRY   PL0259
TITLE   Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE   16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
REFERENCE
          PL0259
          PL0231
          #authors Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
          D.; Marshak-Rothstein, A.; Weigert, M.
          #journal J. Exp. Med. (1990) 171:265-297
          #title   Anti-DNA antibodies from autoimmune mice arise by clonal
          expansion and somatic mutation.
          #cross-references MUID:90111618
          #accession PL0259
          ##molecule_type mRNA
          ##residues 1-106 ##label SHL
          #superfamily immunoglobulin V region; immunoglobulin homology
          heterotetramer; immunoglobulin

CLASSIFICATION
KEYWORDS

FEATURE
          1-23   #region framework 1\
          24-34   #region complementarity-determining 1\
          35-49   #region framework 2\
          50-56   #region complementarity-determining 2\
          57-88   #region framework 3\
          89-97   #region complementarity-determining 3\
          98-106   #region framework 4\
SUMMARY   #length 106 #checksum 2162

Query Match   84.0%; Score 110; DB 2; Length 106;
Best Local Similarity   82.4%; Pred. No. 2.15e-07;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db   30 GSSLNWLQQEPDGTIKR 46
            :|:||:||||||||||||
Qy   50 GINLHWLQQEPDGTIKR 66

Db   30 GSSLNWLQQEPDGTIKR 46
            :|:||:||||||||||||
Qy   50 GINLHWLQQEPDGTIKR 66

Db   52 GSSLNWLQQEPDGTIKR 68
            :|:||:||||||||||||
Qy   50 GINLHWLQQEPDGTIKR 66

RESULT 4

ENTRY   KVMSM4
TITLE   Ig kappa chain precursor V region (MOPC 41) - mouse
CONTAINS Ig kappa chain precursor V region VK41
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE   24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change

---

(Right column)

ACCESSIONS
REFERENCE
          #authors D.; Marshak-Rothstein, A.; Weigert, M.
          #journal J. Exp. Med. (1990) 171:265-297
          #title   Anti-DNA antibodies from autoimmune mice arise by clonal
          expansion and somatic mutation.
          #cross-references MUID:90111618
          PL0260
          #accession PL0259
          ##molecule_type mRNA
          ##residues 1-106 ##label SHL
          #superfamily immunoglobulin V region; immunoglobulin homology
          heterotetramer; immunoglobulin

CLASSIFICATION
KEYWORDS

FEATURE
          1-23   #region framework 1\
          24-34   #region complementarity-determining 1\
          35-49   #region framework 2\
          50-56   #region complementarity-determining 2\
          57-88   #region framework 3\
          89-97   #region complementarity-determining 3\
          98-106   #region framework 4\
SUMMARY   #length 106 #checksum 2157

Query Match   84.0%; Score 110; DB 2; Length 105;
Best Local Similarity   82.4%; Pred. No. 2.15e-07;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

ACCESSIONS
REFERENCE
          #authors Seldman, J.G.; Max, E.E.; Leder, P.
          #journal Nature (1979) 280:370-375
          #title   A kappa-immunoglobulin gene is formed by site-specific
          recombination without further somatic mutation.
          A93211
          #residues 1-117 ##label VK41
          the sequences were determined from the differentiated
          gene MOPC 41 and the germline gene VK41
          #cross-references MUID:79221900

REFERENCE
          A93815
          #authors Burstein, Y.; Schechter, I.
          #journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720
          #title   Amino acid sequence of the NH-2-terminal extra piece segments
          of the precursors of mouse immunoglobulin lambda-1-type and
          kappa-type light chains.
          #cross-references MUID:77148916
          #accession A93815
          ##molecule_type protein
          ##residues 1-33 ##label BUR
          ##residues 23-49,'B',51-53,'LSB',57-58,'ZZ',61-62,'BZ',65-76,'B',
          78-130,110-130 ##label GRA
          #note   Met-3 is apparently used as an alternative initiator in
          25% of the chains

REFERENCE
          A94239
          #authors Gray, W.R.; Dreyer, W.J.; Hood, L.
          #journal Science (1967) 155:465-467
          #title   Mechanism of antibody synthesis: size differences between
          mouse kappa kappa chains.
          #cross-references MUID:67056897
          #accession A94239
          ##molecule_type protein
          ##residues 23-49,'B',51-53,'LSB',57-58,'ZZ',61-62,'BZ',65-76,'B',
          #experimental_source Bence Jones protein MOPC 41

GENETICS
COMPLEX   19/1
          An immunoglobulin heterotetramer subunit consists of two
          identical light (kappa or lambda) and two identical heavy
          (alpha, delta, epsilon, gamma, or mu) chains usually
          stabilized by interchain disulfide bonds. In some cases,
          such as IgA and IgM, the subunits associate into larger
          oligomers.
          #superfamily immunoglobulin V region; immunoglobulin homology
          alternative initiators; heterotetramer; immunoglobulin

CLASSIFICATION
KEYWORDS

FEATURE
          1-22   #domain signal sequence #status experimental #label
                      SIG1\
          3-22   #domain signal sequence #status experimental #label
                      SIG2\
          23-130   #product Ig kappa chain V region (MOPC 41) #status
                      experimental #label M41\
          38-112   #domain immunoglobulin homology #label IMM\
          45-110   #disulfide_bonds #status predicted
SUMMARY   #length 130 #molecular-weight 14311 #checksum 6707

Query Match   84.0%; Score 110; DB 1; Length 130;
Best Local Similarity   82.4%; Pred. No. 2.15e-07;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 5

ENTRY   PH1062
TITLE   Ig light chain V region (clone 202.105) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse

ACCESSIONS
REFERENCE
          A93211; B93211; A93815; A94239; A01922; A01923
          #accession B93211
          ##molecule_type DNA
          ##residues 1-130 ##label PC41
          16-Aug-1996
          A93211
          ##molecule_type DNA
          ##residues 1-130 ##label PC41

DATE   30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                15-Jun-1996
ACCESSIONS   PH0971
REFERENCE   PH1062
  #authors   Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
  #journal   J. Exp. Med. (1992) 176:761-779
  #title   Both IgM and IgG anti-DNA antibodies are the products of
                clonally selective B cell stimulation in (NZB x NZW)F1
                mice.
  #accession   PH1062
    ##status   nucleic acid sequence not shown
    ##molecule_type mRNA
    ##residues 1-98 ##label TIL
    ##experimental_source B cell, strain [NZB x NZW]F1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   immunoglobulin
SUMMARY   #length 98 #checksum 6933

Query Match   71.8%;
Best Local Similarity 85.7%; Score 94; DB 2; Length 98;
Matches   12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db   33 LSWLQQKPDGTIKR 46
        |||| ||||| ||||
Qy   53 LHWLQQEPDGTIKR 66

RESULT 6
ENTRY   PL0262 #type fragment
TITLE   Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
                16-Aug-1996
ACCESSIONS   PL0262
REFERENCE   PL0231
                PL0262
  #authors   Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
                D.; Marshak-Rothstein, A.; Weigert, M.
  #journal   J. Exp. Med. (1990) 171:265-297
  #title   Anti-DNA antibodies from autoimmune mice arise by clonal
                expansion and somatic mutation.
  #cross-references MUID:90111618
  #accession   PL0262
    ##molecule_type mRNA
    ##residues 1-106 ##label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
FEATURE
                1-23   #region framework 1\
                24-34   #region complementarity-determining 1\
                35-49   #region framework 2\
                50-56   #region complementarity-determining 2\
                57-88   #region framework 3\
                89-97   #region complementarity-determining 3\
                98-106 #region framework 4\
SUMMARY   #length 106 #checksum 658

Query Match
Best Local Similarity 85.7%; Score 94; DB 2; Length 106;
Matches   12; Conservative 0; Pred. No. 1.45e-04; Mismatches 2; Indels 0; Gaps 0;

Db   33 LSWLQQKPDGTIKR 46
        |||| ||||| ||||
Qy   53 LHWLQQEPDGTIKR 66

RESULT 7
ENTRY   S17622 #type complete
TITLE   Ig kappa chain V region - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
                09-May-1997
ACCESSIONS   S17622
REFERENCE   S17230
  #authors   Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
  #journal   Nature (1991) 352:624-628
  #title   Making antibody fragments using phage display libraries.
  #cross-references MUID:91326098
  #accession   S17622
    ##status   preliminary
    ##molecule_type nucleic acid
    ##residues 1-91 ##label CLA
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY   #length 91 #molecular-weight 9895 #checksum 3446

Query Match
Best Local Similarity 78.6%; Score 91; DB 2; Length 91;
Matches   11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db   25 LSWLQQKPDGSIKR 38
        |||| ||||| ||||
Qy   53 LHWLQQEPDGTIKR 66

RESULT 8
ENTRY   B47271 #type fragment
TITLE   nitrophenyl phosphonate-specific antibody 48G7 light chain VJ
                - synthetic (fragment)
ORGANISM   Mus musculus (house mouse) gene engineered and expressed in
                Escherichia coli
                #formal_name synthetic
                #note
DATE   21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change
                11-Aug-1995
ACCESSIONS   B47271
REFERENCE   A47271
  #authors   Lesley, S.A.; Patten, P.A.; Schultz, P.G.
  #journal   Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1160-1165
  #title   A genetic approach to the generation of antibodies with
                enhanced catalytic activities.
  #cross-references MUID:93165560
  #accession   B47271
    ##molecule_type protein
    ##residues 1-108 ##label LE5
    ##note   sequence extracted from NCBI backbone (NCBIN:124856,
                NCBIP:124859)
    ##note   parts of this sequence were determined by protein
                sequencing
FEATURE
    ##note   #disulfide_bonds #status predicted
SUMMARY   #length 108 #checksum 9036

Query Match
Best Local Similarity 85.7%; Score 94; DB 2; Length 106;
Matches   12; Conservative 0; Pred. No. 1.45e-04; Mismatches 2; Indels 0; Gaps 0;

Db   34 LGWLQQKPDGTIKR 47
        | |||||||| ||||
Qy   53 LHWLQQEPDGTIKR 66

RESULT 9
ENTRY   D28840 #type fragment
TITLE   Ig kappa chain V region (HP29) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change
                20-Mar-1998
ACCESSIONS   D28840; K25114
REFERENCE   A91028
  #authors   Ollier, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau,
                M.
  #journal   EMBO J. (1985) 4:3681-3688
  #title   The idiotypic network and the internal image: possible
                regulation of a germ-line network by paucigene encoded Ab2
                (anti-idiotypic) antibodies in the GAT system.
  #cross-references MUID:86136012
  #accession   D28840

Query Match
Best Local Similarity 85.7%; Score 91; DB 4; Length 108;
Matches   12; Conservative 0; Pred. No. 4.70e-04; Mismatches 2; Indels 0; Gaps 0;

Db   34 LGWLQQKPDGTIKR 47
        | |||||||| ||||
Qy   53 LHWLQQEPDGTIKR 66

```
                  #molecule_type mRNA
                  ##residues 1-92 ##label OLL
                  #cross-references GB:X03384; NID:g52157; PID:g52158
CLASSIFICATION    #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS          heterotetramer; immunoglobulin
SUMMARY           #length 92 #checksum 7017

Query Match              68.7%;   Score 90;   DB 2;   Length 92;
Best Local Similarity    64.7%;   Pred. No. 6.95e-04;
Matches    11;   Conservative   3;   Mismatches   3;   Indels   0;   Gaps   0;

Db     15   SVYLNWLQQKLDGTIKR 31
            :: |:||| ||||||
Qy     50   GINLHWLQQEPDGTIKR 66


RESULT 10
ENTRY      B28840      #type fragment
TITLE      Ig kappa chain V region (HP27) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change
           16-Aug-1996
ACCESSIONS B28840; I25114
REFERENCE  A91028
           Oller, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau,
           M.
#journal   EMBO J. (1985) 4:3681-3688
#title     The idiotypic network and the internal image: possible
           regulation of a germ-line network by paucigene encoded Ab2
           (anti-idiotypic) antibodies in the GAT system.
#cross-references MUID:86136012
#accession B28840
#molecule_type mRNA
##residues 1-101 ##label OLL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY    #length 101 #checksum 7015

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Best Local Similarity    58.8%;   Pred. No. 6.97e-03;
Matches    10;   Conservative   4;   Mismatches   3;   Indels   0;   Gaps   0;

Db     24   SVYLNWLQRKLDGTIKR 40
            :: |:||| ||||||
Qy     50   GINLHWLQQEPDGTIKR 66


RESULT 11
ENTRY      C28840      #type fragment
TITLE      Ig kappa chain V region (HP22) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change
           16-Aug-1996
ACCESSIONS C28840; J25114
REFERENCE  A91028
           Oller, P.; Rocca-Serra, J.; Somme, G.; Theze, J.; Fougereau,
           M.
The EMBO J. (1985) 4:3681-3688
#title     The idiotypic network and the internal image: possible
           regulation of a germ-line network by paucigene encoded Ab2
           (anti-idiotypic) antibodies in the GAT system.
#cross-references MUID:86136012
#accession C28840
##molecule_type mRNA
##residues 1-101 ##label OLL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY    #length 101 #checksum 5983

Query Match              64.1%;   Score 84;   DB 2;   Length 101;
Best Local Similarity    58.8%;   Pred. No. 6.97e-03;
Matches    10;   Conservative   4;   Mismatches   3;   Indels   0;   Gaps   0;
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Db     24   SVYLNWLQRKLDGTIKR 40
            :: |:||| ||||||
Qy     50   GINLHWLQQEPDGTIKR 66


RESULT 12
ENTRY      S38564      #type fragment
TITLE      Ig kappa chain V region (ASWU1) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
           20-Mar-1998
ACCESSIONS S38564
REFERENCE  S38559
#authors   Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
#submission submitted to the EMBL Data Library, September 1993
#description Molecular analysis of mercury-induced anti-nucleolar
           antibodies in H-2s Mice.
#accession S38564
##status   preliminary
##molecule_type mRNA
##residues 1-93 ##label MON
#cross-references EMBL:X75105; NID:g414153; PID:g414154
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   immunoglobulin
SUMMARY    #length 93 #checksum 1511

Query Match              58.0%;   Score 76;   DB 2;   Length 93;
Best Local Similarity    69.2%;   Pred. No. 1.35e-01;
Matches    9;   Conservative   2;   Mismatches   2;   Indels   0;   Gaps   0;

Db     33   LNWYQQKPDGTVK 45
            :|:|| || |||||
Qy     53   LHWLQQEPDGTIK 65


RESULT 13
ENTRY      PH0087      #type fragment
TITLE      Ig kappa chain V region (anti-cyclosporin C and D) - mouse
           (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change
           20-Mar-1998
ACCESSIONS PH0087
REFERENCE  PH0087
           Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher,
           H.P.; Quesniaux, V.F.J.; Van Regenmortel, M.H.V.
#journal   Mol. Immunol. (1990) 27:1029-1038
#title     Analysis of the structural diversity of monoclonal antibodies
           to cyclosporine.
#cross-references GB:X57639; NID:g296839; PID:g296840
#accession PH0087
##molecule_type mRNA
##residues 1-105 ##label SCH
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
FEATURE
   24-34   #region complementarity-determining 1\
   50-56   #region complementarity-determining 2\
   89-97   #region complementarity-determining 3
SUMMARY    #length 105 #checksum 9783

Query Match              58.0%;   Score 76;   DB 2;   Length 105;
Best Local Similarity    69.2%;   Pred. No. 1.35e-01;
Matches    9;   Conservative   2;   Mismatches   2;   Indels   0;   Gaps   0;

Db     33   LNWYQQKPDGTVK 45
            :|:|| || |||||
Qy     53   LHWLQQEPDGTIK 65


RESULT 14
ENTRY      A48677      #type fragment
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```
TITLE          Ig kappa chain V-J region (48) - mouse (fragment)
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           19-May-1994 #sequence_revision 19-May-1994 #text_change
               20-Mar-1998
ACCESSIONS     A48677
REFERENCE      A48677
#authors       Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb,
               P.; Brown, A.; Hasemann, C.A.; Capra, J.D.; Meek, K.
#journal       Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9508-9512
#title         Molecular characterization of monoclonal CRI-A-positive
               anti-arsonate antibodies derived from idiotype-negative
               mice bearing a light chain polymorphism.
#accession     A48677
##status       preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues     1-107 ##label TAS
CLASSIFICATION
KEYWORDS       #superfamily immunoglobulin v region; immunoglobulin homology
               immunoglobulin
SUMMARY        #length 107 #checksum 7886

Query Match    58.0%;   Score 76; DB 2; Length 107;
Best Local Similarity    69.2%;   Pred. No. 1.35e-01;
Matches     9;   Conservative   2;   Mismatches   2;   Indels   0;   Gaps   0;

Db    33  LNWYQQKPDGTVK 45
          |:|  || ||||:|
Qy    53  LHWLQQEPDGTIK 65


RESULT   15
ENTRY          B48677         #type fragment
TITLE          Ig kappa chain V-J region (44.1) - mouse (fragment)
ORGANISM       #formal_name Mus musculus #common_name house mouse
DATE           19-May-1994 #sequence_revision 19-May-1994 #text_change
               20-Mar-1998
ACCESSIONS     B48677
REFERENCE      B48677
#authors       Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb,
               P.; Brown, A.; Hasemann, C.A.; Capra, J.D.; Meek, K.
#journal       Proc. Natl. Acad. Sci. U.S.A. (1993) 90:9508-9512
#title         Molecular characterization of monoclonal CRI-A-positive
               anti-arsonate antibodies derived from idiotype-negative
               mice bearing a light chain polymorphism.
#accession     B48677
##status       preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues     1-107 ##label TAS
CLASSIFICATION #superfamily immunoglobulin;v region; immunoglobulin homology
KEYWORDS       immunoglobulin
SUMMARY        #length 107 #checksum 9096

Query Match    58.0%;   Score 76; DB 2; Length 107;
Best Local Similarity    69.2%;   Pred. No. 1.35e-01;
Matches     9;   Conservative   2;   Mismatches   2;   Indels   0;   Gaps   0;

Db    33  LNWYQQKPDGTVK 45
          |:|  || ||||:|
Qy    53  LHWLQQEPDGTIK 65


Search completed: Tue Apr 20 13:58:55 1999
Job time : 13 secs.
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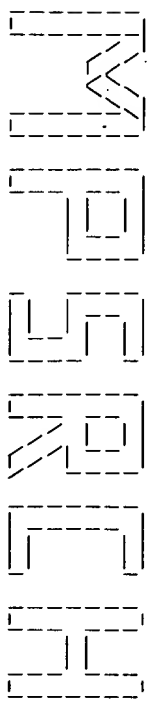
MPSRCH (TM)

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 20 14:04:22 1999; MasPar time 2.65 Seconds
67.085 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-836-455-1_1
Perfect Score: 63
Sequence: 1 MTQSPSSLSAS 11   (24-34) from trans.pep (1 of 3)

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 15.144; Variance 52.220; scale 0.290

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	63	100.0	104	29	W52225	Antibody LD2-4-VL cha	3.52e+00
2	63	100.0	105	29	W52217	Antibody LD1-84-VL ch	3.52e+00
3	63	100.0	105	29	W52239	Antibody LD1-6-17-VL	3.52e+00
4	63	100.0	105	29	W52241	Antibody LD1/2-6-3-VL	3.52e+00
5	63	100.0	105	29	W52219	Antibody LD1-110-VL c	3.52e+00
6	63	100.0	105	29	W52237	Antibody LD2-20-VL ch	3.52e+00
7	63	100.0	105	29	W52233	Antibody LD2-14-VL ch	3.52e+00
8	63	100.0	106	29	W52213	Antibody LD1-40-VL ch	3.52e+00
9	63	100.0	106	29	W52215	Antibody LD1-52-VL ch	3.52e+00
10	63	100.0	106	29	W52227	Antibody LD2-5-VL cha	3.52e+00
11	63	100.0	106	29	W52221	Antibody LD1-117-VL c	3.52e+00
12	63	100.0	106	24	W22412	Humanised alpha-4 int	3.52e+00
13	63	100.0	107	29	W41390	Humanised alpha-4 Int	3.52e+00
14	63	100.0	107	29	W41397	Anti-CEA antibody llg	3.52e+00
15	63	100.0	107	29	W23953	Chimeric humanised 806	3.52e+00
16	63	100.0	107	29	W44123	Light chain variable	3.52e+00
17	63	100.0	107	27	W27568	Anti-TNF-alpha antibo	3.52e+00
18	63	100.0	107	21	W11920	Humanised MAb SK48-E2	3.52e+00
19	63	100.0	107	14	R79247	Light chain variable	3.52e+00
20	63	100.0	107	14	R78972	light chain variable	3.52e+00
21	63	100.0	108	27	W23440	Modified light chain	3.52e+00
22	63	100.0	108	27	W23439	Modified light chain	3.52e+00
23	63	100.0	108	28	W23442	hWI2 light chain.	3.52e+00
24	63	100.0	108	21	W04177	Variant variable ligh	3.52e+00
25	63	100.0	108	5	R28751	Light chain variable	3.52e+00
26	63	100.0	113	29	W42472	Interleukin-5 humanis	3.52e+00
27	63	100.0	117	28	W41147	Human vkappa65.15 fra	3.52e+00
28	63	100.0	126	28	W36164	Humanised light chain	3.52e+00
29	63	100.0	126	14	R76678	Human/murine chimeric	3.52e+00
30	63	100.0	126	14	R76667	Human/murine chimeric	3.52e+00
31	63	100.0	126	14	R76675	Human/murine chimeric	3.52e+00
32	63	100.0	126	14	R76676	Human/murine chimeric	3.52e+00
33	63	100.0	126	14	R76680	Human/murine chimeric	3.52e+00
34	63	100.0	126	19	W04388	Chimeric human/murin	3.52e+00
35	63	100.0	235	29	W31691	Humanised anti-VLA-4	3.52e+00
36	63	100.0	235	28	R90684	Humanized 5C7.29 anti	3.52e+00
37	63	100.0	214	26	W34504	Light chain of human	3.52e+00
38	63	100.0	214	26	W34506	Light chain of full 1	3.52e+00
39	63	100.0	234	21	W11638	Human anti-RSV monocl	3.52e+00
40	63	100.0	235	19	W41411	Human anti-RSV monocl	3.52e+00
41	63	100.0	235	29	W41398	Humanised light chain	3.52e+00
42	63	100.0	235	21	W11640	Human anti-RSV monocl	3.52e+00
43	63	100.0	240	19	W23954	Chimeric humanised Mu	3.52e+00
44	63	100.0	245	19	R98943	Humanised anti-CD38 m	3.52e+00
45	63	100.0	355	28	W35133	R. piplens recombinan	3.52e+00

ALIGNMENTS

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RESULT
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ID   W52225 standard; Protein; 104 AA.
AC   W52225;
DT   12-JUN-1998  (first entry)
DE   Antibody LD2-4-VL chain sequence.
KW   Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW   Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
OS   Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
OS   Homo sapiens.
PN   WO9749809-A1.
PD   31-DEC-1997.
PF   20-JUN-1997; E03253.
PR   24-JUN-1996; EP-810421.
PA   (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI   Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI   Vogel M;
DR   WPI; 98-077173/07.
DR   N-PSDB; V19749.
PT   New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT   Rhesus D antigen in therapy, e.g. for treating idiopathic
PT   thrombocytopenic purpura
PS   Claim 1; Fig 7B; 68pp; English.
CC   This sequence is the antibody LD2-4-VL chain sequence, which is a
CC   polypeptide of the invention. The polypeptides are capable of forming
CC   antigen binding structures with specificity for Rhesus D antigens which
CC   include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC   variable heavy (VH) and variable light (VL) chain sequences. The
CC   antibodies are active against the Rhesus D antigen. They can be used for
CC   treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC   e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC   protection of Rhesus negative women before or immediately after the birth
CC   of a Rhesus positive child to prevent haemolytic disease of the newborn
CC   (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC   immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC   to Rhesus negative recipients in order to prevent sensitisation to the
CC   Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ   Sequence 104 AA;

Query Match        100.0%;  Score 63;  DB 29;  Length 104;
Best Local Similarity  100.0%;  Pred. No. 3.52e+00;
Matches   11;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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Db
Qy   2 mtqspsslsas 12
      ||||||||||||
      24 MTQSPSSLSAS 34

```
RESULT 2
ID   W52217 standard; Protein; 105 AA.
AC   W52217;
DT   12-JUN-1998 (first entry)
DE   Antibody LD1-84-VL chain sequence.
KW   Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW   Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW   idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
OS   Homo sapiens.
PN   WO9749809-A1.
PD   31-DEC-1997.
PF   20-JUN-1997; EP-810421.
PR   24-JUN-1996; EP-810421.
PA   (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI   Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI   Vogel M;
DR   N-PSDB; V19741.
DR   WPI; 98-077173/07.
PT   New Rhesus D antigen in therapy, e.g. for treating idiopathic
PT   thrombocytopenic purpura
PS   Claim 1; Fig 3B; 68pp; English.
CC   This sequence is the antibody LD1-84-VL chain sequence, which is a
CC   polypeptide of the invention. The polypeptides are capable of forming
CC   antigen binding structures with specificity for Rhesus D antigens which
CC   include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC   variable heavy (VH) and variable light (VL) chain sequences. The
CC   antibodies are active against the Rhesus D antigen. They can be used for
CC   treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC   e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC   protection of Rhesus negative child to prevent haemolytic disease of the newborn
CC   (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC   immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC   to Rhesus negative recipients in order to prevent sensitisation to the
CC   Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ   Sequence 105 AA;

Query Match            100.0%;  Score 63;  DB 29;  Length 105;
Best Local Similarity 100.0%;  Pred. No. 3.52e+00;
Matches  11;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    2 mtqspsslsas 12
        ||||||||||||
      24 MTQSPSSLSAS 34


RESULT 3
ID   W52239 standard; Protein; 105 AA.
AC   W52239;
DT   12-JUN-1998 (first entry)
DE   Antibody LD1-6-17-VL chain sequence.
KW   Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW   Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW   idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
OS   Homo sapiens.
PN   WO9749809-A1.
PD   31-DEC-1997.
PF   20-JUN-1997; EP-810421.
PR   24-JUN-1996; EP-810421.
PA   (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI   Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI   Vogel M;
DR   N-PSDB; V19763.
DR   WPI; 98-077173/07.
PT   New Rhesus D antigen in therapy, e.g. for treating idiopathic
PT   thrombocytopenic purpura
```

```
PS   Claim 1; Fig 14B; 68pp; English.
CC   This sequence is the antibody LD1-6-17-VL chain sequence, which is a
CC   polypeptide of the invention. The polypeptides are capable of forming
CC   antigen binding structures with specificity for Rhesus D antigens which
CC   include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC   variable heavy (VH) and variable light (VL) chain sequences. The
CC   antibodies are active against the Rhesus D antigen. They can be used for
CC   treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC   e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC   protection of Rhesus negative child to prevent haemolytic disease of the newborn
CC   (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC   immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC   to Rhesus negative recipients in order to prevent sensitisation to the
CC   Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ   Sequence 105 AA;

Query Match            100.0%;  Score 63;  DB 29;  Length 105;
Best Local Similarity 100.0%;  Pred. No. 3.52e+00;
Matches  11;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db
Qy    2 mtqspsslsas 12
        ||||||||||||
      24 MTQSPSSLSAS 34


RESULT 4
ID   W52241 standard; Protein; 105 AA.
AC   W52241;
DT   12-JUN-1998 (first entry)
DE   Antibody LD1/2-6-3-VL chain sequence.
KW   Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW   Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW   idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
OS   Homo sapiens.
PN   WO9749809-A1.
PD   31-DEC-1997.
PF   20-JUN-1997; EP-810421.
PR   24-JUN-1996; EP-810421.
PA   (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI   Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI   Vogel M;
DR   N-PSDB; V19765.
DR   WPI; 98-077173/07.
PT   New Rhesus D antigen in therapy, e.g. for treating idiopathic
PT   thrombocytopenic purpura
PS   Claim 1; Fig 15B; 68pp; English.
CC   This sequence is the antibody LD1/2-6-3-VL chain sequence, which is a
CC   polypeptide of the invention. The polypeptides are capable of forming
CC   antigen binding structures with specificity for Rhesus D antigens which
CC   include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC   variable heavy (VH) and variable light (VL) chain sequences. The
CC   antibodies are active against the Rhesus D antigen. They can be used for
CC   treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC   e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC   protection of Rhesus negative child to prevent haemolytic disease of the newborn
CC   (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC   immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC   to Rhesus negative recipients in order to prevent sensitisation to the
CC   Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ   Sequence 105 AA;

Query Match            100.0%;  Score 63;  DB 29;  Length 105;
Best Local Similarity 100.0%;  Pred. No. 3.52e+00;
Matches  11;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db
Qy    2 mtqspsslsas 12
        ||||||||||||
      24 MTQSPSSLSAS 34
```

RESULT 5

```
ID   W52219 standard; Protein; 105 AA.
AC   W52219;
DT   12-JUN-1998 (first entry)
DE   Antibody LD1-110-VL chain sequence.
KW   Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW   Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW   idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
OS   Homo sapiens.
PN   WO9749809-A1.
PD   31-DEC-1997.
PF   20-JUN-1996; EP-810421.
PR   24-JUN-1996; EP-810421.
PA   (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI   Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI   Vogel M;
DR   WPI; 98-077173/07.
DR   N-PSDB; V19743.
PT   New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT   Rhesus D antigen in therapy, e.g. for treating idiopathic
PT   thrombocytopenic purpura
CC   Claim 1; Fig 4B; 68pp; English.
CC   This sequence is the antibody LD1-110-VL chain sequence, which is a
CC   polypeptide of the invention. The polypeptides are capable of forming
CC   antigen binding structures with specificity for Rhesus D antigens which
CC   include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC   variable heavy (VH) and variable light (VL) chain sequences. The
CC   antibodies are active against the Rhesus D antigen. They can be used for
CC   treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC   e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC   protection of Rhesus negative child to prevent haemolytic disease of the
CC   of a Rhesus positive women before or immediately after the birth
CC   (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC   immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC   to Rhesus negative recipients in order to prevent sensitisation to the
CC   Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ   Sequence 105 AA.

  Query Match             100.0%;  Score 63; DB 29; Length 105;
  Best Local Similarity   100.0%;         Pred. No. 3.52e+00;
  Matches   11;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          24 MTQSPSSLSAS 34
               |||||||||||
Db           2 mtgspsslsas 12
```

RESULT 6

```
ID   W52237 standard; Protein; 105 AA.
AC   W52237;
DT   12-JUN-1998 (first entry)
DE   Antibody LD2-20-VL chain sequence.
KW   Antibody; variable light chain; VL chain;
KW   Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW   idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
OS   Homo sapiens.
PN   WO9749809-A1.
PD   31-DEC-1997.
PF   20-JUN-1996; EP-810421.
PR   24-JUN-1996; EP-810421.
PA   (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI   Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI   Vogel M;
DR   WPI; 98-077173/07.
DR   N-PSDB; V19761.
PT   New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT   Rhesus D antigen in therapy, e.g. for treating idiopathic
PT   thrombocytopenic purpura
CC   Claim 1; Fig 13B; 68pp; English.
CC   This sequence is the antibody LD2-20-VL chain sequence, which is a
CC   polypeptide of the invention. The polypeptides are capable of forming
CC   antigen binding structures with specificity for Rhesus D antigens which
CC   include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC   variable heavy (VH) and variable light (VL) chain sequences. The
CC   antibodies are active against the Rhesus D antigen. They can be used for
CC   treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC   e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC   protection of Rhesus negative child to prevent haemolytic disease of the newborn
CC   of a Rhesus positive women before or immediately after the birth
CC   (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC   immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC   to Rhesus negative recipients in order to prevent sensitisation to the
CC   Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ   Sequence 105 AA.

  Query Match             100.0%;  Score 63; DB 29; Length 105;
  Best Local Similarity   100.0%;         Pred. No. 3.52e+00;
  Matches   11;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          24 MTQSPSSLSAS 34
               |||||||||||
Db           2 mtgspsslsas 12
```

RESULT 7

```
ID   W52233 standard; Protein; 105 AA.
AC   W52233;
DT   12-JUN-1998 (first entry)
DE   Antibody LD2-14-VL chain sequence.
KW   Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW   Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW   idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
OS   Homo sapiens.
PN   WO9749809-A1.
PD   31-DEC-1997.
PF   20-JUN-1996; EP-810421.
PR   24-JUN-1996; EP-810421.
PA   (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI   Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI   Vogel M;
DR   WPI; 98-077173/07.
DR   N-PSDB; V19757.
PT   New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT   Rhesus D antigen in therapy, e.g. for treating idiopathic
PT   thrombocytopenic purpura
CC   Claim 1; Fig 11B; 68pp; English.
CC   This sequence is the antibody LD2-14-VL chain sequence, which is a
CC   polypeptide of the invention. The polypeptides are capable of forming
CC   antigen binding structures with specificity for Rhesus D antigens which
CC   include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC   variable heavy (VH) and variable light (VL) chain sequences. The
CC   antibodies are active against the Rhesus D antigen. They can be used for
CC   treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC   e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC   protection of Rhesus negative child to prevent haemolytic disease of the newborn
CC   of a Rhesus positive women before or immediately after the birth
CC   (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC   immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC   to Rhesus negative recipients in order to prevent sensitisation to the
CC   Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ   Sequence 105 AA.

  Query Match             100.0%;  Score 63; DB 29; Length 105;
  Best Local Similarity   100.0%;         Pred. No. 3.52e+00;
  Matches   11;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          24 MTQSPSSLSAS 34
               |||||||||||
Db           2 mtgspsslsas 12
```

RESULT 8

```
ID   W52213 standard; Protein; 106 AA.
AC   W52213;
DT   12-JUN-1998 (first entry)
DE   Antibody LD1-40-VL chain sequence.
```

Column 1

KW Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
OS Homo sapiens.
PN WO9749809-A1.
PD 31-DEC-1997;
PF 20-JUN-1997; E03253.
PR 24-JUN-1996; EP-810421.
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI Vogel M;
DR WPI: 98-077173/07.
DR N-PSDB; V19737.
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura
PS Claim 1; Fig 1B; 68pp; English.
CC This sequence is the antibody LD1-40-VL chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after to prevent mistransfusions of Rhesus D
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ Sequence 106 AA;

Query Match   100.0%;   Score 63;   DB 29;   Length 106;
Best Local Similarity 100.0%;   Pred. No. 3.52e+00;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Db        2 mtgspsslsas 12
            |||||||||||
Qy       24 MTQSPSSLSAS 34
```

Column 2

RESULT 9
ID W52215 standard; protein; 106 AA.
AC W52215;
DT 12-JUN-1998 (first entry)
    Antibody LD1-52-VL chain sequence.
    Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
    Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
OS Homo sapiens.
PN WO9749809-A1.
PD 31-DEC-1997;
PF 20-JUN-1997; E03253.
PR 24-JUN-1996; EP-810421.
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI Vogel M;
DR WPI: 98-077173/07.
DR N-PSDB; V19739.
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura
PS Claim 1; Fig 2B; 68pp; English.
CC This sequence is the antibody LD1-52-VL chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after to prevent mistransfusions of Rhesus D
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ Sequence 106 AA;

Query Match   100.0%;   Score 63;   DB 29;   Length 106;
Best Local Similarity 100.0%;   Pred. No. 3.52e+00;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Db        2 mtgspsslsas 12
            |||||||||||
Qy       24 MTQSPSSLSAS 34
```

Column 3

CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after to prevent mistransfusions of Rhesus D
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ Sequence 106 AA;

Query Match   100.0%;   Score 63;   DB 29;   Length 106;
Best Local Similarity 100.0%;   Pred. No. 3.52e+00;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db        2 mtgspsslsas 12
            |||||||||||
Qy       24 MTQSPSSLSAS 34
```

RESULT 10
ID W52227 standard; protein; 106 AA.
AC W52227;
DT 12-JUN-1998 (first entry)
DE Antibody LD2-5-VL chain sequence.
DE Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
OS Homo sapiens.
PN WO9749809-A1.
PD 31-DEC-1997;
PF 20-JUN-1997; E03253.
PR 24-JUN-1996; EP-810421.
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI Vogel M;
DR WPI: 98-077173/07.
DR N-PSDB; V19751.
PT New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT Rhesus D antigen in therapy, e.g. for treating idiopathic
PT thrombocytopenic purpura
PS Claim 1; Fig 8B; 68pp; English.
CC This sequence is the antibody LD2-5-VL chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after to prevent mistransfusions of Rhesus D
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ Sequence 106 AA;

Query Match   100.0%;   Score 63;   DB 29;   Length 106;
Best Local Similarity 100.0%;   Pred. No. 3.52e+00;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Db        2 mtgspsslsas 12
            |||||||||||
Qy       24 MTQSPSSLSAS 34
```

RESULT 11
ID W52221 standard; protein; 106 AA.
AC W52221;
DT 12-JUN-1998 (first entry)
DE Antibody LD1-117-VL chain sequence.
DE Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
OS Homo sapiens.
PN WO9749809-A1.

PD   31-DEC-1997.
PF   20-JUN-1997; E03253.
PR   24-JUN-1996; EP-810421.
PA   (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
PI   Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
PI   Vogel M;
DR   WPI: 98-077173/07.
DR   N-PSDB: V19745.
PN   New Rhesus D antigen binding poly:peptide(s) - used to neutralise
PT   Rhesus D antigen in therapy e.g. for treating idiopathic
PT   thrombocytopenic purpura.
PS   Claim 1; Fig 5B; 68pp; English.
CC   This sequence is the antibody LD1-117-VL chain sequence, which is a
CC   polypeptide of the invention. The polypeptides are capable of forming
CC   antigen binding structures with specificity for Rhesus D antigens which
CC   include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC   variable heavy (VH) and variable light (VL) chain sequences. The
CC   antibodies are active against the Rhesus D antigen. They can be used for
CC   treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC   e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC   protection of Rhesus negative women before or immediately after the birth
CC   of a Rhesus positive child to prevent haemolytic disease of the newborn
CC   (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC   immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC   to Rhesus negative recipients in order to prevent sensitisation to the
CC   Rhesus D antigen. The products can also be used as diagnostic reagents.
SQ   Sequence 106 AA;

Qy   24 MTQSPSSLSAS 34

Query Match   100.0%; Score 63; DB 29; Length 106;
Best Local Similarity   100.0%; Pred. No. 3.52e+00;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   2 mtqspsslsas 12

RESULT 12
ID   W22412 standard; Protein; 106 AA.
AC   W22412;
DT   08-DEC-1997 (first entry)
DE   Humanised alpha-4 integrin antibody 21.6 VL La.
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
FH   Key   Location/Qualifiers
FT   region   1..23
FT   /label= FR1
FT   /note= "REI framework region 1"
FT   region   24..34
FT   /label= CDR1
FT   /note= "21.6 complementarity determining region 1"
FT   region   35..49
FT   /label= FR2
FT   /note= "REI framework region 2"
FT   misc_difference 45
FT   /note= "REI Lys-45 is substd. by Lys of mouse
FT   CDR2 loop"
FT   misc_difference 49
FT   /note= "REI Tyr-49 is substd. by His of mouse
FT   located at the binding site"
FT   region   50..56
FT   /label= CDR2
FT   /note= "21.6 complementarity determining region 2"
FT   region   57..88
FT   /label= FR3
FT   /note= "REI framework region 3"
FT   misc_difference 58
FT   /note= "REI Val-58 is substd. by Ile of mouse
FT   21.6 VL, important in supporting the CDR2
FT   loop"
FT   misc_difference 69
FT   /note= "REI Thr-69 is substd. by Arg of mouse
FT   21.6 VL, involved in antibody-antigen
FT   binding"
FT   region   89..96
FT   /label= FR4
FT   /note= "REI framework region 4"
FT   region   97..106
FT   /label= CDR3
FT   /note= "21.6 complementarity determining region 3"
FT   misc_difference 103
FT   /note= "REI Leu-103 substd. by Val, more typical
FT   of human kappa light chain J region"
FT   misc_difference 104
FT   /note= "REI Gln-104 substd. by Glu, more typical
FT   of human kappa light chain J region"
FT   misc_difference 106
FT   /note= "REI Thr-106 substd. by Lys, more typical
FT   of human kappa light chain J region"
PN   WO9718838-A1.
PD   29-MAY-1997.
PF   21-NOV-1996; U18807.
PR   21-NOV-1995; US-561521.
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
PI   Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
WPI: 97-297879/27.
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
PS   Claim 25; Fig 6; 107pp; English.
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6. It is
CC   composed of complementarity determining regions (CDRs) from the VL
CC   region (see W22409) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human REI framework. It can be expressed in
CC   mammalian host cells following PCR amplification and mutagenesis
CC   of appropriate fragments of mouse and human DNA sequences. The
CC   humanised 21.6 VL and a humanised 21.6 VH (see W22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury. The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen. It is also useful for
CC   generating idiotypic antibodies. The humanised antibody has a
CC   half-life in the human circulation essentially equivalent to that
CC   of naturally occurring human antibodies.
SQ   Sequence 106 AA;

Qy   24 MTQSPSSLSAS 34

Query Match   100.0%; Score 63; DB 24; Length 106;
Best Local Similarity   100.0%; Pred. No. 3.52e+00;
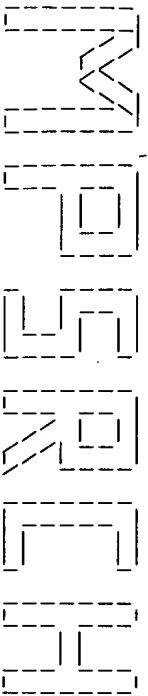Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   4 mtqspsslsas 14

RESULT 13
ID   W41390 standard; Protein; 107 AA.
AC   W41390;
DT   02-JUN-1998 (first entry)
DE   Anti-CEA antibody light chain variable region VK4.
KW   Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW   cancer diagnosis; complementarity determining region; light chain.
OS   Synthetic.
PN   WO9742329-A1.

RESULT 14

ID   W41397 standard; Protein; 107 AA.
AC   W41397;
DT   02-JUN-1998 (first entry)
DE   Anti-CEA antibody 806.077 variable light chain.
KW   Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
KW   cancer diagnosis; complementarity determining region; Fd chain.
OS   Chimeric - Homo sapiens.
OS   Chimeric - Mus sp.
PN   WO9742329-A1.
PD   13-NOV-1997.
PD   29-APR-1997;
PF   14-FEB-1997; GB-003103.
PR   04-MAY-1996; GB-009405.
PA   (ZENE) ZENECA LTD.
PI   Copley CG, Edge MD, Emery SC;
PT   WPI; 97-558987/51.
PT   N-PSDB; V17296.
PT   Anti-carcinoembryonic antigen antibody 806.077 Ab - used for
PT   diagnosis and therapy of cancer
PS   Example 11; Page 122-123; 208pp; English.
CC   This sequence is the light chain variable region of the antibody of
CC   the invention. The antibody is an anti-CEA (carcinoembryonic antigen)
CC   antibody (806.077 Ab). Host cells or transgenic organisms transformed
CC   with DNA encoding the antibody, are used to make the antibody or
CC   conjugate. The conjugate is used in a medicament suitable for intravenous
CC   administration. The conjugate can be used for cancer therapy, selectively
CC   killing tumour cells. The antibody can be used for in vivo or in vitro
CC   diagnosis of cancer.
SQ   Sequence 107 AA;

Query Match   100.0%; Score 63; DB 29; Length 107;
Best Local Similarity 100.0%; Pred. No. 3.52e+00;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   4 mtqspsslsas 14
             |||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 15

ID   W23953 standard; Protein; 107 AA.
AC   W23953;

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 M P S R C H (TM)
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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

on on: Tue Apr 20 14:03:38 1999;   MasPar time 3.28 Seconds
                                            125.736 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-836-455-1_1
                 (24-34) from trans.pep (1 of 3)
Perfect Score: 63
Sequence: 1 MTQSPSSLSAS 11

Scoring table: PAM 150
                 Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: pir58
                 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 21.222; Variance 25.990; scale 0.817

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                    SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description	Pred. No.
1	63	100.0	53	2	PH0881	Ig kappa chain V regi	1.28e-03
2	63	100.0	53	2	PH0879	Ig kappa chain V regi	1.28e-03
3	63	100.0	62	2	S42265	Ig lambda chain V reg	1.28e-03
4	63	100.0	94	2	PH1063	Ig light chain V regi	1.28e-03
5	63	100.0	97	2	PH1064	Ig light chain V regi	1.28e-03
6	63	100.0	103	2	S26332	Ig light chain V regi	1.28e-03
7	63	100.0	104	2	S26330	Ig kappa chain V regi	1.28e-03
8	63	100.0	106	2	PC2397	anti-tetanus toxin 9F	1.28e-03
9	63	100.0	106	2	C33936	Ig kappa chain V regi	1.28e-03
10	63	100.0	106	2	PL0259	Ig kappa chain V regi	1.28e-03
11	63	100.0	106	2	PL0260	Ig kappa chain V regi	1.28e-03
12	63	100.0	107	2	S40366	Ig kappa chain V-J re	1.28e-03
13	63	100.0	107	2	S36275	Ig kappa chain V reg	1.28e-03
14	63	100.0	107	2	S35262	Ig lambda chain V reg	1.28e-03
15	63	100.0	107	2	S35269	Ig lambda chain V reg	1.28e-03
16	63	100.0	107	2	JT0139	Ig lambda chain V reg	1.28e-03
17	63	100.0	108	2	S36279	Ig kappa chain V regi	1.28e-03
18	63	100.0	109	2	S31983	Ig lambda chain V reg	1.28e-03
19	63	100.0	109	2	S31998	Ig kappa chain - huma	1.28e-03
20	63	100.0	109	2	S31979	Ig kappa chain - huma	1.28e-03
21	63	100.0	109	2	S31981	Ig kappa chain - huma	1.28e-03
22	63	100.0	109	2	S32001	Ig kappa chain - huma	1.28e-03
23	63	100.0	110	2	S44118	Ig kappa chain V-J re	1.28e-03
24	63	100.0	116	2	A27594	Ig kappa chain precur	1.28e-03
25	63	100.0	117	2	S42263	Ig kappa chain V regi	1.28e-03
26	63	100.0	117	2	S41809	Ig kappa chain V regi	1.28e-03
27	63	100.0	117	2	S21668	Ig kappa chain V regi	1.28e-03
28	63	100.0	117	2	S42264	Ig kappa chain V regi	1.28e-03
29	63	100.0	117	2	S24206	Ig kappa chain V regi	1.28e-03
30	63	100.0	117	2	C21056	Ig kappa chain precur	1.28e-03
31	63	100.0	117	2	B21056	Ig kappa chain precur	1.28e-03
32	63	100.0	120	2	S21666	Ig kappa chain V regi	1.28e-03
33	63	100.0	120	2	S21667	Ig kappa chain V regi	1.28e-03
34	63	100.0	122	2	S40314	Ig kappa chain - huma	1.28e-03
35	63	100.0	122	2	S40354	Ig kappa chain V regi	1.28e-03
36	63	100.0	123	2	S40331	Ig kappa chain V-J re	1.28e-03
37	63	100.0	123	2	S40313	Ig kappa chain V regi	1.28e-03
38	63	100.0	123	2	S09365	Ig kappa chain - mous	1.28e-03
39	63	100.0	125	2	S40350	Ig kappa chain V-J-C	1.28e-03
40	63	100.0	125	2	S40353	Ig kappa chain V regi	1.28e-03
41	63	100.0	125	2	S40315	Ig kappa chain - huma	1.28e-03
42	63	100.0	126	2	S21056	Ig kappa chain precur	1.28e-03
43	63	100.0	127	2	S40335	Ig kappa chain V-J-C	1.28e-03
44	63	100.0	129	2	S40367	Ig kappa chain V-J-C	1.28e-03
45	63	100.0	135	2	S24320	Ig kappa chain precur	1.28e-03

                    ALIGNMENTS

RESULT   1
ENTRY   PH0881   #type fragment
TITLE   Ig kappa chain V region (GOU) - human (fragment)
ALTERNATE_NAMES myeloma protein
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change
                 09-May-1997
ACCESSIONS   PH0881
REFERENCE   PH0881
                 #authors Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.;
                 Smith, A.; Diamond, B.
                 J. Exp. Med. (1991) 174:1639-1652
                 #journal   Molecular characteristics of antibodies bearing an
                 #title   anti-DNA-associated idiotype.
                 #cross-references MUID:92078875
                 #accession PH0881
                 ##residues 1-53 ##label MAN
                 ##molecule_type protein
CLASSIFICATION   #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
FEATURE
                 1-23   #region framework 1\
                 24-34   #region complementarity-determining 1\
                 35-49   #region framework 2\
                 50-53   #region complementarity-determining 2
SUMMARY   #length 53   #checksum 237

Query Match   Best Local Similarity 100.0%;   Score 63; DB 2; Length 53;
Matches 11; Conservative 0; Pred. No. 1.28e-03; Mismatches 0; Indels 0; Gaps 0;

Qy   24 MTQSPSSLSAS 34
            |||||||||||
Db   4 MTQSPSSLSAS 14

RESULT   2
ENTRY   PH0879   #type fragment
TITLE   Ig kappa chain V region (MAR) - human (fragment)
ALTERNATE_NAMES myeloma protein
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change
                 09-May-1997
ACCESSIONS   PH0879
REFERENCE   PH0862
                 #authors Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.;
                 Smith, A.; Diamond, B.
```

RESULT 3

ENTRY   S42265   #type complete
TITLE   Ig kappa chain V region (018) - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
             09-May-1997
ACCESSIONS   S42265
REFERENCE   S42265
             S42263
#authors   Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.;
             Schaeble, K.F.; Thiebe, R.; Quenzel, E.M.; Zachau, H.G.;
             Nahm, M.H.
#journal   J. Immunol. (1991) 147:4007-4013
#title   Clonal characterization of the human IgG antibody repertoire
             to Haemophilus influenzae type b polysaccharide. IV. The
             less frequently expressed VL are heterogenous.
#accession   S42265
             ##status preliminary
             ##molecule_type DNA
             ##residues 1-62 ##label SCO
             ##cross-references EMBL:M64856

GENETICS
#introns   19/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
WORDS   #length 62 #molecular-weight 6821 #checksum 8574

Query Match 100.0%; Score 63; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.28e-03;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   24 MTQSPSSLSAS 34

Db   4 MTQSPSSLSAS 14
          |||||||||||
Qy   24 MTQSPSSLSAS 34

#journal   J. Exp. Med. (1991) 174:1639-1652
#title   Molecular characteristics of antibodies bearing an
             anti-DNA-associated idiotype.
#cross-references MUID:92078875
#accession   PH0879
             #molecule_type protein
             ##residues 1-57 ##label MAN
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
FEATURE
1-23   #region framework 1\
24-34   #region complementarity-determining 1\
35-49   #region framework 2\
50-56   #region complementarity-determining 2
SUMMARY   #length 57 #checksum 6305

Query Match 100.0%; Score 63; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.28e-03;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   24 MTQSPSSLSAS 34

RESULT 4

ENTRY   PH1063   #type fragment
TITLE   Ig light chain V region (clone 202.33) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
             15-Jun-1996
ACCESSIONS   PH1063
REFERENCE   PH0971
             PH1063
#authors   Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
#journal   J. Exp. Med. (1992) 176:761-779
#title   Both IgM and IgG anti-DNA antibodies are the products of
             clonally selective B cell stimulation in (NZB x NZW)F1
             mice.

Matches   11; Conservative   0; Pred. No. 1.28e-03;

Db   4 MTQSPSSLSAS 14
          |||||||||||
Qy   24 MTQSPSSLSAS 34

#accession   PH1063
             ##status nucleic acid sequence not shown
             ##molecule_type mRNA
             ##residues 1-94 ##label TIL
#experimental_source B cell, strain [NZB x NZW]F1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   immunoglobulin
SUMMARY   #length 94 #checksum 1938

Query Match 100.0%; Score 63; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.28e-03;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   24 MTQSPSSLSAS 34

Db   4 MTQSPSSLSAS 14
          |||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 5

ENTRY   PH1064   #type fragment
TITLE   Ig light chain V region (clone 202.54) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
             15-Jun-1996
ACCESSIONS   PH1064
REFERENCE   PH0971
             PH1064
#authors   Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
#journal   J. Exp. Med. (1992) 176:761-779
#title   Both IgM and IgG anti-DNA antibodies are the products of
             clonally selective B cell stimulation in (NZB x NZW)F1
             mice.
#accession   PH1064
             ##status nucleic acid sequence not shown
             ##molecule_type mRNA
             ##residues 1-97 ##label TIL
#experimental_source B cell, strain [NZB x NZW]F1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   immunoglobulin
SUMMARY   #length 97 #checksum 1339

Query Match 100.0%; Score 63; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.28e-03;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   24 MTQSPSSLSAS 34

Db   4 MTQSPSSLSAS 14
          |||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 6

ENTRY   S26332   #type fragment
TITLE   Ig light chain V region - mouse (fragment)
ALTERNATE_NAMES Ig kappa chain V region
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change
             03-Aug-1998
ACCESSIONS   S26332; S26331
REFERENCE   S26309
             S26332; S26331
#authors   Stark, S.E.; Caton, A.J.
#journal   J. Exp. Med. (1991) 174:613-624
#title   Antibodies that are specific for a single amino acid
             interchange in a protein epitope use structurally distinct
             variable regions.
#accession   S26332
             ##molecule_type mRNA
             ##residues 1-103 ##label STA
             ##cross-references EMBL:X59187; NID:g52318; PID:e36167; PID:g1334064
             ##note the sequence of residues 1-8 and the corresponding
             nucleic acid sequence are not shown
#accession   S26331
             ##status preliminary
             ##molecule_type mRNA
             ##residues 1-103 ##label ST2

CLASSIFICATION #cross-references EMBL:X59191; NID:g52321; PID:e36171; PID:g1334066
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 103 #checksum 1197

Query Match 100.0%; Score 63; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.28e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy  24 MTQSPSSLSAS 34
       |||||||||||
Db   4 MTQSPSSLSAS 14
```

RESULT 7
ENTRY S26330 #type complete
TITLE Ig kappa chain V region - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
08-Sep-1997
ACCESSIONS S26330
REFERENCE S26330
#authors Stark, S.E.; Caton, A.J.
#journal J. Exp. Med. (1991) 174:613-624
#title Antibodies that are specific for a single amino acid
interchange in a protein epitope use structurally distinct
variable regions.
#accession S26330
##status preliminary
##molecule_type mRNA
##residues 1-104 ##label STA
#cross-references EMBL:X59185; NID:g52316; PID:e36165; PID:g1334063
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 104 #molecular-weight 11443 #checksum 4741

Query Match 100.0%; Score 63; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.28e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy  24 MTQSPSSLSAS 34
       |||||||||||
Db   4 MTQSPSSLSAS 14
```

RESULT 8
ENTRY PC2397 #type fragment
TITLE anti-tetanus toxin 9912 Fab light-chain - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
16-Feb-1997
ACCESSIONS PC2397
REFERENCE PC2397
#authors Esposito, G.; Scarselli, E.; Traboni, C.
#journal Gene (1994) 148:167-168
#title Phage display of a human antibody against Clostridium tetani
toxin.
#accession PC2397
##molecule_type mRNA
##residues 1-106 ##label ESP
#cross-references EMBL:X75387
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
24-34 #region complementarity determining region 1\
50-56 #region complementarity determining region 2
SUMMARY #length 106 #checksum 4925

Query Match 100.0%; Score 63; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.28e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Db   4 MTQSPSSLSAS 14
       |||||||||||
```

```
Qy  24 MTQSPSSLSAS 34
```

RESULT 9
ENTRY C33936 #type fragment
TITLE Ig kappa chain V region (VM113) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change
08-Sep-1997
ACCESSIONS C33936
REFERENCE C33936
#authors Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:4664-4668
#title Nucleotide changes in sequential variants of influenza virus
hemagglutinin genes and molecular structures of
corresponding monoclonal antibodies specific for each
variant.
#accession C33936
##status preliminary
##molecule_type mRNA
##residues 1-106 ##label MEE
#cross-references MUID:89282831
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 106 #checksum 2278

Query Match 100.0%; Score 63; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.28e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Db   4 MTQSPSSLSAS 14
       |||||||||||
Qy  24 MTQSPSSLSAS 34
```

RESULT 10
ENTRY PL0259 #type fragment
TITLE Ig kappa chain V region (anti-DNA, D11VK) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
16-Aug-1996
ACCESSIONS PL0259
PL0231
REFERENCE PL0259
#authors Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
D.; Marshak-Rothstein, A.; Weigert, M.
#journal J. Exp. Med. (1990) 171:265-297
#title Anti-DNA antibodies from autoimmune mice arise by clonal
expansion and somatic mutation.
#accession PL0259
##molecule_type mRNA
##residues 1-106 ##label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-23 #region framework 1\
24-34 #region complementarity-determining 1\
35-49 #region framework 2\
50-56 #region complementarity-determining 2\
57-88 #region framework 3\
89-97 #region complementarity-determining 3\
98-106 #region framework 4
SUMMARY #length 106 #checksum 2162

Query Match 100.0%; Score 63; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.28e-03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Db   4 MTQSPSSLSAS 14
       |||||||||||
Qy  24 MTQSPSSLSAS 34
```

RESULT 11

ENTRY   PL0260   #type fragment
TITLE   Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE   16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
REFERENCE   16-Aug-1996
ACCESSIONS   PL0260
             PL0231
#authors   Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky,
             D.; Marshak-Rothstein, A.; Weigert, M.
#journal   J. Exp. Med. (1990) 171:265-297
#title   Anti-DNA antibodies from autoimmune mice arise by clonal
             expansion and somatic mutation.
#cross-references MUID:9011618
#accession   PL0260
##molecule_type mRNA
##residues   1-106
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
FEATURE
    1-23   #region framework 1\
   24-34   #region complementarity-determining 1\
   35-49   #region framework 2\
   50-56   #region complementarity-determining 2\
   57-88   #region framework 3\
   89-97   #region complementarity-determining 3\
   98-106   #region framework 4
SUMMARY   #length 106 #checksum 2157

Query Match   100.0%;   Score 63; DB 2;   Length 106;
Best Local Similarity 100.0%;   Pred. No. 1.28e-03;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   4 MTQSPSSLSAS 14
           |||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 12

ENTRY   S40366   #type complete
TITLE   Ig kappa chain V-J region - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   19-May-1994 #sequence_revision 26-May-1995 #text_change
REFERENCE   20-Mar-1998
ACCESSIONS   S40366
             S40312
#authors   Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal   Eur. J. Immunol. (1993) 23:3248-3271
#title   Expressed human immunoglobulin chi genes and their
             hypermutation.
#accession   S40366
##status   preliminary; translation not shown
##molecule_type mRNA
##residues   1-107 ##label KLE
CLASSIFICATION EMBL:X72476; NID:g441420; PID:g441421
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY   #length 107 #molecular-weight 11556 #checksum 9149

Query Match   100.0%;   Score 63; DB 2;   Length 107;
Best Local Similarity 100.0%;   Pred. No. 1.28e-03;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   4 MTQSPSSLSAS 14
           |||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 13

ENTRY   S36275   #type fragment
TITLE   Ig lambda chain V region (clone alpha-FOG1-A4) - human

ORGANISM   #formal_name Homo sapiens #common_name man
DATE   03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
             08-Sep-1997
ACCESSIONS   S36275
             S36256
REFERENCE   S36255
#authors   Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
             Embleton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;
             Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
             G.
#journal   EMBO J. (1993) 12:725-734
#title   Human anti-self antibodies with high specificity from phage
             display libraries.
#accession   S36275
##status   preliminary; nucleic acid sequence not shown
##molecule_type mRNA
##residues   1-107 ##label GRI
CLASSIFICATION EMBL:Z18827; NID:g33416; PID:g939909
KEYWORDS   #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY   heterotetramer; immunoglobulin
             #length 107 #checksum 8985

Query Match   100.0%;   Score 63; DB 2;   Length 107;
Best Local Similarity 100.0%;   Pred. No. 1.28e-03;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   4 MTQSPSSLSAS 14
           |||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 14

ENTRY   S36262   #type fragment
TITLE   Ig lambda chain V region (clone alpha-TNF-E7) - human
             (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
             16-Aug-1996
ACCESSIONS   S36262
REFERENCE   S36256
             S36255
#authors   Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
             Embleton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;
             Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
             G.
#journal   EMBO J. (1993) 12:725-734
#title   Human anti-self antibodies with high specificity from phage
             display libraries.
#accession   S36262
##status   preliminary; nucleic acid sequence not shown
##molecule_type mRNA
##residues   1-107 ##label GRI
CLASSIFICATION EMBL:Z18842
KEYWORDS   #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY   heterotetramer; immunoglobulin
             #length 107 #checksum 4341

Query Match   100.0%;   Score 63; DB 2;   Length 107;
Best Local Similarity 100.0%;   Pred. No. 1.28e-03;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   4 MTQSPSSLSAS 14
           |||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 15

ENTRY   S36269   #type fragment
TITLE   Ig lambda chain V region (clone alpha-TNF-A1) - human
             (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
             08-Sep-1997
ACCESSIONS   S36269
REFERENCE   S36256
             S36255

#authors   Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
            Embleton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;
            Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
            G.
#journal   EMBO J. (1993) 12:725-734
#title   Human anti-self antibodies with high specificity from phage
            display libraries.
#accession S36269
##status   preliminary; nucleic acid sequence not shown
##molecule_type mRNA
##residues 1-107 ##label GRI
##cross-references EMBL:Z18838; NID:g933422; PID:g939915
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS   heterotetramer; immunoglobulin
SUMMARY   #length 107 #checksum 6368

Query Match   100.0%;   Score 63; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.28e-03;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   4 MTQSPSSLSAS 14
            |||||||||||
Db   24 MTQSPSSLSAS 34

Search completed: Tue Apr 20 14:04:04 1999
Job time : 26 secs.

```
**********************************************************
*                                                        *
*                  MPSRCH  (TM)                          *
*                                                        *
**********************************************************

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```

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 20 14:02:18 1999; MasPar time 2.40 Seconds
                     ---122.815 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-836-455-1_1
Perfect Score: (24-34) from trans.pep (1 of 3)
Sequence: 63
                      1 MTQSPSSLSAS 11

Scoring table: PAM 150
                      Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%
                      Listing first 45 summaries

Database: swiss-prot35
                      1:swissprot

Statistics: Mean 21.723; Variance 21.843; scale 0.994

                      Pred. No. is the number of results predicted by chance to have a
                      score greater than or equal to the score of the result being printed,
                      and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	63	100.0	108	1	KV1Y_HUMAN	IG KAPPA CHAIN V-I REG	1.78e-05
2	63	100.0	108	1	KV1Q_HUMAN	IG KAPPA CHAIN V-I REG	4.67e-05
3	63	100.0	108	1	KV1P_HUMAN	IG KAPPA CHAIN V-I REG	4.67e-05
4	63	100.0	108	1	KV1X_HUMAN	IG KAPPA CHAIN V-I REG	4.67e-05
5	63	100.0	108	1	KV1G_HUMAN	IG KAPPA CHAIN V-I REG	4.67e-05
6	63	100.0	108	1	KV1O_HUMAN	IG KAPPA CHAIN V-I REG	4.67e-05
7	63	100.0	108	1	KV1N_HUMAN	IG KAPPA CHAIN V-I REG	4.67e-05
8	63	100.0	108	1	KV1R_HUMAN	IG KAPPA CHAIN V-I REG	4.67e-05
9	63	100.0	108	1	KV1E_HUMAN	IG KAPPA CHAIN V-I REG	4.67e-05
10	63	100.0	108	1	KV1A_HUMAN	IG KAPPA CHAIN V-I REG	4.67e-05
11	63	100.0	108	1	KV1B_HUMAN	IG KAPPA CHAIN V-I REG	4.67e-05
12	63	100.0	109	1	KV1T_HUMAN	IG KAPPA CHAIN V-I REG	4.67e-05
13	63	100.0	108	1	KV5H_MOUSE	IG KAPPA CHAIN PRECURS	4.67e-05
14	63	100.0	117	1	KV1I_HUMAN	IG KAPPA CHAIN V-I REG	4.67e-05
15	63	100.0	129	1	KV1X_HUMAN	IG KAPPA CHAIN PRECURS	4.67e-05
16	63	100.0	129	1	KV1W_HUMAN	IG KAPPA CHAIN PRECURS	4.67e-05
17	63	100.0	130	1	KV5G_MOUSE	IG KAPPA CHAIN PRECURS	4.67e-05
18	61	96.8	107	1	KV1D_HUMAN	IG KAPPA CHAIN V-I REG	1.78e-04
19	61	96.8	108	1	KV5P_MOUSE	IG KAPPA CHAIN V-V REG	1.78e-04
20	61	96.8	108	1	KV1F_HUMAN	IG KAPPA CHAIN V-I REG	1.78e-04
21	61	96.8	108	1	KV5O_MOUSE	IG KAPPA CHAIN V-V REG	1.78e-04
22	61	96.8	112	1	KV1U_HUMAN	IG KAPPA CHAIN V-I REG	1.78e-04
23	61	96.8	115	1	KV5C_MOUSE	IG KAPPA CHAIN PRECURS	1.78e-04
24	61	96.8	117	1	KV1J_HUMAN	IG KAPPA CHAIN PRECURS	1.78e-04
25	60	95.2	108	1	KV1C_HUMAN	IG KAPPA CHAIN V-I REG	3.46e-04
26	59	93.7	108	1	KV1M_HUMAN	IG KAPPA CHAIN V-I REG	6.67e-04
27	58	92.1	108	1	KV5K_MOUSE	IG KAPPA CHAIN V-V REG	1.28e-03
28	58	92.1	108	1	KV5Q_MOUSE	IG KAPPA CHAIN V-V REG	1.28e-03
29	58	92.1	108	1	KV5R_MOUSE	IG KAPPA CHAIN V-V REG	1.28e-03
30	58	92.1	108	1	KV5T_MOUSE	IG KAPPA CHAIN V-V REG	1.28e-03
31	57	90.5	109	1	KV5J_MOUSE	IG KAPPA CHAIN V-V REGIO	1.28e-03
32	56	88.9	114	1	KV01_RAT	IG KAPPA CHAIN V-V REGIO	2.44e-03
33	56	88.9	121	1	KV1K_HUMAN	IG KAPPA CHAIN V-I REG	2.44e-03
34	55	87.3	108	1	KV1S_HUMAN	IG KAPPA CHAIN V-I REG	4.62e-03
35	55	87.3	108	1	KV1V_HUMAN	IG KAPPA CHAIN V-I REG	4.62e-03
36	55	87.3	129	1	KV5M_MOUSE	IG KAPPA CHAIN PRECURS	4.62e-03
37	53	84.1	108	1	KV5L_MOUSE	IG KAPPA CHAIN V-V REG	8.70e-03
38	53	84.1	108	1	KV5N_MOUSE	IG KAPPA CHAIN V-V REG	8.70e-03
39	53	84.1	108	1	KV5U_MOUSE	IG KAPPA CHAIN V-V REG	8.70e-03
40	53	84.1	108	1	KV5S_MOUSE	IG KAPPA CHAIN V-V REG	8.70e-03
41	53	84.1	109	1	KV01_RAT	IG KAPPA CHAIN V-V REGIO	8.70e-03
42	53	84.1	114	1	KV4A_HUMAN	IG KAPPA CHAIN V-IV RE	3.03e-02
43	53	84.1	121	1	KV4O_HUMAN	IG KAPPA CHAIN V-IV RE	3.03e-02
44	53	84.1	133	1	KV4B_HUMAN	IG KAPPA CHAIN PRECURS	3.03e-02
45	53	84.1	134	1	KV4C_HUMAN	IG KAPPA CHAIN PRECURS	3.03e-02
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ALIGNMENTS

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RESULT 1

ID   KV1Y_HUMAN      STANDARD;      PRT;      108 AA.
AC   P80362;
DT   01-NOV-1995 (REL. 32, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (WAT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE; 95086080.
RA   HUANG D.-B., CHANG C.-H., AINSWORTH C., BRUENGER A.T., EULITZ M.,
RA   SOLOMON A., STEVENS F.J., SCHIFFER M.;
RL   BIOCHEMISTRY 33:14848-14857(1994).
RN   [2]
RP   SEQUENCE OF 1-35.
RX   MEDLINE; 81267384.
RA   STEVENS F.J., WESTHOLM F.A., PANAGIOTOPOULOS N., SCHIFFER M.,
RA   POPP R.A., SOLOMON A.;
RL   J. MOL. BIOL. 147:185-193(1981).
CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PDB; 1WTL; 01-NOV-94.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; 3D-STRUCTURE.
FT   DOMAIN           1     23    FRAMEWORK 1.
FT   DOMAIN          24     34    COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN          35     49    FRAMEWORK 2.
FT   DOMAIN          50     56    COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN          57     88    FRAMEWORK 3.
FT   DOMAIN          89     97    COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN          98    107    FRAMEWORK 4.
FT   DISULFID        23     88    BY SIMILARITY.
FT   CONFLICT        30     31    IN -> SD (IN REF. 2).
FT   NON_TER        108    108
SQ   SEQUENCE  108 AA;  11737 MW;  41A2388C CRC32;
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Query Match       100.0%;  Score 63;  DB 1;  Length 108;
Best Local Similarity  100.0%;  Pred. No. 4.67e-05;
Matches     11;  Conservative     0;  Mismatches     0;  Indels     0;  Gaps     0;

Qy        4 MTQSPSSLSAS 14
            |||||||||||
Db       24 MTQSPSSLSAS 34
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RESULT   2

ID   KV1Q_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01609;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (SCW).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
     SEQUENCE.
RA   HILSCHMANN N.;
     MEDLINE; 75059271.
RA   HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:842-866(1974).
RL   EULITZ M., HILSCHMANN N.;
CC   -!- THIS IS A BENCE-JONES PROTEIN.
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
DR   PIR; A01875; KIHUSW.
DR   HSSP; P01607; 1IGM.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   107   FRAMEWORK 4.
FT   DISULFID   23   88   BY SIMILARITY.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA;   11764 MW; 66DABC95 CRC32;

Query Match   100.0%; Score 63; DB 1; Length 108;
Best Local Similarity   100.0%; Pred. No. 4.67e-05;
  Matches   11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   4 MTQSPSSLSAS 14
              |||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 3
ID   KV1P_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (ROY).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
     SEQUENCE.
RA   MEDLINE; 68362076.
RA   HILSCHMANN N.;
RX   HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 348:1077-1080(1967).
RN   [2]
RP   REVISIONS TO 39 AND 41.
RL   HILSCHMANN N., BARNIKOL H.U., HESS M., LANGER B., PONSTINGL H.,
RA   STEINMETZ-KAYNE M., SUTER L., WATANABE S.;
RA   (IN) GAMMA GLOBULINS: STRUCTURE AND FUNCTION, FRANEK F., SHUGAR D.,
     EDS., PP. 57-74, ACADEMIC PRESS, NEW YORK, (1969).
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01874; KIHURY.
HSSP; P01607; 1IGM.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   107   FRAMEWORK 4.
FT   DISULFID   23   88   BY SIMILARITY.

RESULT 4
ID   KV1G_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01599;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (GAL).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
     SEQUENCE.
RA   MEDLINE; 75059122.
RA   LAURE C.J., WATANABE S., HILSCHMANN N.;
RL   HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 354:1503-1504(1973).
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
DR   PIR; A01867; KIHUGL.
DR   HSSP; P01607; 1DFB.
KW   IMMUNOGLOBULIN V REGION.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   107   FRAMEWORK 4.
FT   DISULFID   23   88   BY SIMILARITY.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA;   11782 MW; 98778875 CRC32;

Query Match   100.0%; Score 63; DB 1; Length 108;
Best Local Similarity   100.0%; Pred. No. 4.67e-05;
  Matches   11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db   4 MTQSPSSLSAS 14
              |||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 5
ID   KV1O_HUMAN   STANDARD;   PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (REI).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
     SEQUENCE.
RA   MEDLINE; 76023758.
RA   PALM W., HILSCHMANN N.;
RL   HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RA   MEDLINE; 76039968.
RA   EPP O., LATTMAN E.E., SCHIFFER M., HUBER R., PALM W.;
RL   BIOCHEMISTRY 14:4943-4952(1975).
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.

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CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01873; KIHURE.
DR   PDB; 1REI; 17-FEB-84.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN; 3D-STRUCTURE.
FT   DOMAIN         1     23       FRAMEWORK 1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    107       FRAMEWORK 4.
FT   DISULFID      23     88
FT   NON_TER      108    108
FT   STRAND         4      7
FT   STRAND        10     13
FT   TURN          15     16
FT   STRAND        19     25
FT   TURN          30     31
FT   STRAND        33     38
FT   TURN          40     41
FT   STRAND        45     49
FT   TURN          50     52
FT   STRAND        53     54
FT   TURN          56     57
FT   STRAND        60     61
FT   TURN          62     67
FT   STRAND        68     69
FT   STRAND        70     75
FT   HELIX         80     82
FT   STRAND        85     90
FT   STRAND        98     98
FT   STRAND       102    106
SQ   SEQUENCE    108 AA;   11902 MW;  D08F51A4 CRC32;

Query Match    100.0%;     Score 63;   DB 1;  Length 108;
Best Local Similarity 100.0%;   Pred. No. 4.67e-05;   Mismatches 0;   Indels 0;   Gaps 0;
Matches  11;   Conservative  0;

Db    4  MTQSPSSLSAS  14
         |||||||||||
Qy   24  MTQSPSSLSAS  34

RESULT 6
ID   KVIN_HUMAN     STANDARD;    PRT;   108 AA.
AC   P01606;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (OU).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 70201507.
RA   KOHLER H., SHIMIZU A., PAUL C., PUTNAM F.W.;
RL   SCIENCE 169:56-59(1970).
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
DR   PIR; A01872; K1HUOU.
HSSP; P01607; 2FGW.
KW   IMMUNOGLOBULIN V REGION.
FT   DOMAIN         1     23       FRAMEWORK 1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    107       FRAMEWORK 4.
FT   DISULFID      23     88
FT   NON_TER      108    108
SQ   SEQUENCE    108 AA;   11777 MW;  4B089785 CRC32;
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Query Match    100.0%;     Score 63;   DB 1;  Length 108;
Best Local Similarity 90.9%;   Pred. No. 4.67e-05;   Mismatches 0;   Indels 0;   Gaps 0;
Matches  10;   Conservative  1;

Db    4  MTZSPSSLSAS  14
         |:||||||||||
Qy   24  MTQSPSSLSAS  34

RESULT 7
ID   KVIR_HUMAN     STANDARD;    PRT;   108 AA.
AC   P01610;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (WEA).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 83273707.
RA   GONI F., FRANGIONE B.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 80:4837-4841(1983).
CC   -!- THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST
CC       3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC       WALDENSTROM'S MACROGLOBULINEMIA.
DR   PIR; A01876; K1HUWE.
HSSP; P01607; 2FGW.
KW   IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY.
FT   DOMAIN         1     23       FRAMEWORK 1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    107       FRAMEWORK 4.
FT   DISULFID      23     88
FT   NON_TER      108    108
SQ   SEQUENCE    108 AA;   11840 MW;  B8ADA251 CRC32;

Query Match    100.0%;     Score 63;   DB 1;  Length 108;
Best Local Similarity 100.0%;   Pred. No. 4.67e-05;   Mismatches 0;   Indels 0;   Gaps 0;
Matches  11;   Conservative  0;

Db    4  MTQSPSSLSAS  14
         |||||||||||
Qy   24  MTQSPSSLSAS  34

RESULT 8
ID   KVIE_HUMAN     STANDARD;    PRT;   108 AA.
AC   P01597;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (DEE).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 72053133.
RA   MILSTEIN C.P., DEVERSON E.V.;
RL   BIOCHEM. J. 123:945-958(1971).
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR   PIR; A01865; K1HUDE.
HSSP; P01607; 1FVC.
KW   IMMUNOGLOBULIN V REGION.
FT   DOMAIN         1     23       FRAMEWORK 1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
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FT   DOMAIN        50     56      COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88      FRAMEWORK 3.
FT   DOMAIN        89     97      COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    107      FRAMEWORK 4.
FT   DISULFID      23     88
FT   NON_TER      108    108      BY SIMILARITY.
SQ   SEQUENCE     108 AA;  11661 MW;  1DE844F3 CRC32;

Db           4 MTQSPSSLSAS 14
               |||||||||||
Qy          24 MTQSPSSLSAS 34

Query Match             100.0%;  Score 63;  DB 1;  Length 108;
Best Local Similarity   100.0%;  Pred. No. 4.67e-05;
Matches    11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


RESULT 9
KV1A_HUMAN      STANDARD;     PRT;    108 AA.
ID   P01593;
AC
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (AG).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 69234734.
RA   TITANI K., SHINODA T., PUTNAM F.W.;
RL   J. BIOL. CHEM. 244:3550-3560(1969).
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01861; KIHUAG.
DR   HSSP; P01607; 1REI.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT   DOMAIN        1      23      FRAMEWORK 1.
FT   DOMAIN        24     34      COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49      FRAMEWORK 2.
FT   DOMAIN        50     56      COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88      FRAMEWORK 3.
FT   DOMAIN        89     97      COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    107      FRAMEWORK 4.
FT   DISULFID      23     88
FT   NON_TER      108    108
SQ   SEQUENCE     108 AA;  11992 MW;  225444C7 CRC32;

Qy          24 MTQSPSSLSAS 34


RESULT 10
KV1H_HUMAN      STANDARD;     PRT;    108 AA.
ID   P01600;
AC
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (HAU).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 71032830.
RA   WATANABE S., HILSCHMANN N.;
RL   HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1291-1295(1970).
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
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CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01868; KIHUHU.
DR   HSSP; P01607; 1FVC.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT   DOMAIN        1      23      FRAMEWORK 1.
FT   DOMAIN        24     34      COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49      FRAMEWORK 2.
FT   DOMAIN        50     56      COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88      FRAMEWORK 3.
FT   DOMAIN        89     97      COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    107      FRAMEWORK 4.
FT   DISULFID      23     88
FT   NON_TER      108    108      BY SIMILARITY.
SQ   SEQUENCE     108 AA;  11671 MW;  C8A2EE86 CRC32;

Db           4 MTQSPSSLSAS 14
               |||||||||||
Qy          24 MTQSPSSLSAS 34

Query Match             100.0%;  Score 63;  DB 1;  Length 108;
Best Local Similarity   100.0%;  Pred. No. 4.67e-05;
Matches    11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


RESULT 11
KV1B_HUMAN      STANDARD;     PRT;    108 AA.
ID   P01594;
AC
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (AU).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 72189444.
RA   SCHIECHL H., HILSCHMANN N.;
RL   HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE; 77022433.
RA   FEHLHAMMER H., SCHIFFER M., EPP O., COLMAN P.M., LATTMAN E.E.,
RA   SCHWAGER P., STEIGEMANN W., SCHRAMM H.J.;
RL   BIOPHYS. STRUCT. MECH. 1:139-146(1975).
CC   -!- THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR
CC       REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF
CC       THE KAPPA CHAIN REI.
CC   -!- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01862; KIHUAU.
DR   HSSP; P01607; 1IGM.
KW   IMMUNOGLOBULIN V REGION; BENCE-JONES PROTEIN.
FT   DOMAIN        1      23      FRAMEWORK 1.
FT   DOMAIN        24     34      COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49      FRAMEWORK 2.
FT   DOMAIN        50     56      COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88      FRAMEWORK 3.
FT   DOMAIN        89     97      COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    107      FRAMEWORK 4.
FT   DISULFID      23     88
FT   NON_TER      108    108      BY SIMILARITY.
SQ   SEQUENCE     108 AA;  11939 MW;  B455AF00 CRC32;

Qy          24 MTQSPSSLSAS 34

Db           4 MTQSPSSLSAS 14
               |||||||||||
Qy          24 MTQSPSSLSAS 34

Query Match             100.0%;  Score 63;  DB 1;  Length 108;
Best Local Similarity   100.0%;  Pred. No. 4.67e-05;
Matches    11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

RESULT 12

ID   KVIT_HUMAN   STANDARD;   PRT;   109 AA.
AC   P01612;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-I REGION (MEV).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 83081018.
RA   EULITZ M., LINKE R.P.;
RL   HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 363:1347-1358(1982).
CC   -!- ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO FOUND.
CC   -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01879; KIHUMV.
DR   HSSP; P01607; 2FGW.
FT   IMMUNOGLOBULIN V REGION.
FT   DOMAIN   1   23
FT   DOMAIN   24   34   FRAMEWORK-1.
FT   DOMAIN   35   49   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   50   56   FRAMEWORK 2.
FT   DOMAIN   57   88   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   89   98   FRAMEWORK 3.
FT   DOMAIN   99   108   COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID   23   88   FRAMEWORK 4.
FT   NON_TER   109   109   BY SIMILARITY.
SQ   SEQUENCE   109 AA;   11870 MW; D724ECE1 CRC32;

Query Match   100.0%;
Best Local Similarity 100.0%;   Score 63; DB 1; Length 109;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   4 MTQSPSSLSAS 14
          ||||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 13

ID   KV5H_MOUSE   STANDARD;   PRT;   117 AA.
AC   P01641;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 173B).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 81064681.
RA   MAX E.E., SEIDMAN J.G., MILLER H., LEDER P.;
RL   CELL 21:793-799(1980).
DR   EMBL; K00880; G197444; -.
DR   PIR; A01924; KVMS3B.
DR   HSSP; P01607; 1FGV.
KW   IMMUNOGLOBULIN V REGION; SIGNAL.
FT   SIGNAL   1   22
FT   CHAIN   23   117   IG KAPPA CHAIN V-V REGION (MOPC 173B).
FT   DOMAIN   23   45   FRAMEWORK 1.
FT   DOMAIN   46   56   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   57   71   FRAMEWORK 2.
FT   DOMAIN   72   78   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   79   110   FRAMEWORK 3.
FT   DOMAIN   111   >117   COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID   45   110
FT   NON_TER   117   117   BY SIMILARITY.
SQ   SEQUENCE   117 AA;   12954 MW; 38F2B08C CRC32;

Query Match   100.0%;
Best Local Similarity 100.0%;   Score 63; DB 1; Length 117;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   26 MTQSPSSLSAS 36
          ||||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 14

ID   KVII_HUMAN   STANDARD;   PRT;   117 AA.
AC   P01601;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-I REGION (HK101) (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 81098966.
RA   BENTLEY D.L., RABBITTS T.H.;
RL   NATURE 288:730-733(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 83129397.
RA   BENTLEY D.L., RABBITS T.H.;
RL   CELL 32:181-189(1983).
DR   EMBL; J00244; G185970; -.
DR   EMBL; K01322; G185994; -.
DR   EMBL; K01324; G185998; -.
DR   EMBL; V00558; G33177; -.
DR   PIR; A01881; KIHU11.
DR   PIR; A21056; A21056.
DR   HSSP; P01607; 1DFB.
KW   IMMUNOGLOBULIN V REGION; SIGNAL.
FT   SIGNAL   1   22
FT   CHAIN   23   >117   IG KAPPA CHAIN V-I REGION (HK101).
FT   DOMAIN   23   45   FRAMEWORK 1.
FT   DOMAIN   46   56   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   57   71   FRAMEWORK 2.
FT   DOMAIN   72   78   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   79   110   FRAMEWORK 3.
FT   DOMAIN   111   >117   COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID   45   110
FT   NON_TER   117   117   BY SIMILARITY.
SQ   SEQUENCE   117 AA;   12799 MW; B02D3EA1 CRC32;

Query Match   100.0%;
Best Local Similarity 100.0%;   Score 63; DB 1; Length 117;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   26 MTQSPSSLSAS 36
          ||||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 15

ID   KV1X_HUMAN   STANDARD;   PRT;   129 AA.
AC   P04432;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT   01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-I REGION (DAUDI).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85014148.
RA   KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;
RL   NUCLEIC ACIDS RES. 12:6995-7006(1984).
DR   EMBL; K02134; G155822; -.
DR   EMBL; X00966; G296685; ALT_TERM.
DR   EMBL; X00966; G296685; ALT_TERM.

```
DR   PIR; A01884; KIHUDI.
DR   HSSP; P01607; 1FGV.
KW   IMMUNOGLOBULIN V REGION; SIGNAL.
FT   SIGNAL      1     22
FT   CHAIN      23    129      IG KAPPA CHAIN V-I REGION (DAUDI).
FT   DOMAIN     23     45      FRAMEWORK 1.
FT   DOMAIN     46     56      COMPLEMENTARITY-DETERMING 1.
FT   DOMAIN     57     71      FRAMEWORK 2.
FT   DOMAIN     72     78      COMPLEMENTARITY-DETERMING 2.
FT   DOMAIN     79    110      FRAMEWORK 3.
FT   DOMAIN    111    119      COMPLEMENTARITY-DETERMING 3.
FT   DOMAIN    120    129      FRAMEWORK 4.
FT   DISULFID   45    110      BY SIMILARITY.
FT   NON_TER    45
FT   NON_TER   129
SO   SEQUENCE  129 AA;   14235 MW;   05B40B5E CRC32;
```

```
Query Match                100.0%;   Score 63;   DB 1;   Length 129;
Best Local Similarity      100.0%;   Pred. No. 4.67e-05;
Matches    11;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

DB       26 MTQSPSSLSAS 36
            |||||||||||
Qy       24 MTQSPSSLSAS 34
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Search completed: Tue Apr 20 14:02:24 1999
Job time : 6 secs.

MPSRCH (TM)

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 20 14:02:43 1999; MasPar time 4.27 Seconds
                                                128.383 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-836-455-1_1
                   (24-34) from trans.pep (1 of 3)
Perfect Score: 63
Sequence: 1 MTQSPSSLSAS 11

Scoring table: PAM 150
                   Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%
                   Listing first 45 summaries

Database: sptrembl6
                   1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
                   5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
                   9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
                   13:sp_vertebrate 14:sp_virus

Statistics: Mean 20.775; Variance 22.138; scale 0.938

                   Pred. No. is the number of results predicted by chance to have a
                   score greater than or equal to the score of the result being printed,
                   and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	63	100.0	50	4	Q15533	DNA REARRANGED BY A T(	1.08e-04
2	63	100.0	105	4	Q99514	SINGLE-CHAIN FV FRAGME	1.08e-04
3	63	100.0	113	4	043689	ANTI-HER3 SCFV (FRAGME	3.94e-04
4	63	100.0	241	11	P97771	HRV FAB 027-VL (FRAGME	7.47e-04
5	63	100.0	107	4	014540	ANTI-CEA 79 SINGLE CHA	9.20e-03
6	63	100.0	113	4	099953	VASOACTIVE INTESTINAL	1.08e-04
7	63	100.0	117	4	099818	ANTI-SSDNA ANTIBODY LI	1.70e-02
8	61	96.8	102	11	P97408	TYPE II COLLAGEN ANTIB	3.13e-02
9	61	96.8	113	4	015358	IMMUNOGLOBULIN VARIABL	1.08e-04
10	61	96.8	116	4	Q61196	ANTI-CARCINOMA EMBRYON	3.13e-02
11	61	96.8	239	4	014535	HRV FAB N6-VL (FRAGMEN	3.94e-04
12	61	96.8	133	11	Q61551	CC49 FAB PRECURSOR (FR	5.71e-02
13	61	96.8	240	4	Q15982	RHEUMATOID FACTOR C6 L	3.94e-04
14	61	96.8	133	11	035842	ANTI-HIV-1 REVERSE TRA	5.71e-02
15	61	96.8	244	4	043690	ANTI-MPL SCFV (FRAGMEN	3.94e-04
16	61	96.8	262	11	014539	HRV FAB 026-VL (FRAGME	5.71e-02
17	61	96.8	244	4	000289	SINGLE-CHAIN FV FRAGME	3.94e-04
18	61	96.8	113	4	Q99822	ANTI-HIV-1 GP120 ANTIB	1.06e+00
19	61	96.8	244	4	000288	SINGLE-CHAIN FV FRAGME	3.94e-04
20	61	96.8	244	4	00289		
21	48	76.2	134	4	000619	REV25-2 (FRAGMENT).	1.06e+00
22	48	76.2	100	4	Q15535	V KAPPA (FRAGMENT).	3.23e+00
23	46	73.0	115	4	Q99826	ANTI-HIV-1 GP120 V3 LO	3.23e+00
24	46	73.0	358	5	062124	D1025.1.	3.23e+00
25	46	73.0	421	3	043068	HYPOTHETICAL 47.7 KD P	3.23e+00
26	46	71.4	118	4	015986	RHEUMATOID FACTOR D5 L	5.57e+00
27	46	71.4	119	11	055115	IG KAPPA CHAIN PRECURS	5.57e+00
28	45	71.4	119	11	055117	IG KAPPA CHAIN (FRAGME	5.57e+00
29	45	71.4	119	11	055116	IG KAPPA CHAIN (FRAGME	5.57e+00
30	45	71.4	330	2	052370	HRPJ3.	5.57e+00
31	45	69.8	99	11	P97409	TYPE II COLLAGEN ANTI-	9.55e+00
32	44	69.8	107	11	035538	KAPPA (FRAGMENT).	9.55e+00
33	44	69.8	115	4	014537	HRV FAB N27-VL (FRAGME	9.55e+00
34	44	69.8	131	4	Q99671	MONOCLONAL ANTIBODY KA	9.55e+00
35	44	69.8	357	5	062028	CO6B3.9.	9.55e+00
36	44	69.8	441	3	013337	PUTATIVE TRANSCRIPTION	9.55e+00
37	44	69.8	665	10	Q38795	ACETOLACTATE SYNTHASE	9.55e+00
38	44	69.8	741	11	061985	NUCLEAR FACTOR, ERYTHR	9.55e+00
39	44	69.8	904	11	008971	BM28 HOMOLOGUE.	9.55e+00
40	44	69.8	952	13	Q07494	TYROSINE KINASE CEK6 R	9.55e+00
41	44	69.8	1258	4	000539	NUCLEAR PROTEIN SA-1.	9.55e+00
42	43	68.3	127	11	061251	ANTIGEN, B-CELL RECEPT	1.62e+01
43	43	68.3	383	5	016306	T21H3.5 PROTEIN.	1.62e+01
44	43	68.3	463	2	Q49869	PUTATIVE UREASE OPERON	1.62e+01
45	43	68.3	1517	2	034071	ORF40.	1.62e+01

ALIGNMENTS

RESULT 1

ID	Q15533;			PRELIMINARY;	PRT;	50 AA.

AC   Q15533;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   DNA REARRANGED BY A T(2;8) TRANSLOCATION LEADING TO BURKITT'S LYMPHOMA
DE   IN THE CELL LINE JI (CLONE JIP).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KLOBECK H.G.;
RL   SUBMITTED (AUG-1987) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE OF 36-50 FROM N.A.
RX   MEDLINE; 87259967.
RA   KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;
RL   NUCLEIC ACIDS RES. 15:4877-4888(1987).
DR   EMBL; X05929; E12675; -.
SQ   SEQUENCE 50 AA; 5486 MW; 65586C19 CRC32;

Query Match   100.0%;   Score 63; DB 4; Length 50;
Best Local Similarity 100.0%;   Pred. No. 1.08e-04;
Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   7 MTQSPSSLSAS 17
               |||||||||||
Qy   24 MTQSPSSLSAS 34

RESULT 2

ID	Q99514;			PRELIMINARY;	PRT;	105 AA.

AC   Q99514;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   LIGHT CHAIN FAB FRAGMENT (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.

```
RA   HORN M.P., VOGEL M., BIAGGI C., MIESCHER S.M., STADLER B.M.;
RL   SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; Y08148; E274854; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER
FT   NON_TER
SQ   SEQUENCE   105 AA;  11303 MW;  249B7EC3 CRC32;

Db   2 MTQSPSSLSAS 12
       ||||||||||||
Qy  24 MTQSPSSLSAS 34

Query Match       100.0%;  Score 63;  DB 4;  Length 105;
Best Local Similarity 100.0%;  Pred. No. 1.08e-04;
Matches  11;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 3
ID   Q99980           PRELIMINARY;      PRT;   107 AA.
AC   Q99980;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED).
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   VASOACTIVE INTESTINAL POLYPEPTIDE HYDROLYZING AUTOANTIBODY LIGHT CHAIN
DE   (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   TYUTYULKOVA S., GAO Q.S., THOMPSON A., RENNARD S., PAUL S.;
RX   MEDLINE; 96375171.
RL   BIOCHIM. BIOPHYS. ACTA 1316:217-223(1996).
DR   EMBL; L43498; G1850120; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER          1         1
SQ   SEQUENCE   107 AA;  11825 MW;  C1E164AA CRC32;

Db   4 MTQSPSSLSAS 14
       ||||||||||||
Qy  24 MTQSPSSLSAS 34

Query Match       100.0%;  Score 63;  DB 4;  Length 107;
Best Local Similarity 100.0%;  Pred. No. 1.08e-04;
Matches  11;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 4
ID   Q99953           PRELIMINARY;      PRT;   107 AA.
AC   Q99953;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED).
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   VASOACTIVE INTESTINAL POLYPEPTIDE HYDROLYZING AUTOANTIBODY LIGHT CHAIN
DE   (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96375171.
RA   TYUTYULKOVA S., GAO Q.S., THOMPSON A., RENNARD S., PAUL S.;
RL   BIOCHIM. BIOPHYS. ACTA 1316:217-223(1996).
DR   EMBL; L43499; G1850134; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER          1         1
SQ   SEQUENCE   107 AA;  11468 MW;  3D1FEE15 CRC32;

Query Match       100.0%;  Score 63;  DB 4;  Length 107;
Best Local Similarity 100.0%;  Pred. No. 1.08e-04;
Matches  11;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
Db   4 MTQSPSSLSAS 14
       ||||||||||||
Qy  24 MTQSPSSLSAS 34

RESULT 5
ID   O13358           PRELIMINARY;      PRT;   117 AA.
AC   O13358;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED).
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   IMMUNOGLOBULIN VARIABLE REGION, KAPPA LIGHT CHAIN (FRAGMENT).
     VKLA.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BLOOD;
RA   JUUL L., HOUGS L., BARINGTON T.;
RL   SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; Y14865; E1169998; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER          1         1
SQ   SEQUENCE   117 AA;  12748 MW;  03408 1EF CRC32;

Db  26 MTQSPSSLSAS 36
       ||||||||||||
Qy  24 MTQSPSSLSAS 34

Query Match       100.0%;  Score 63;  DB 4;  Length 117;
Best Local Similarity 100.0%;  Pred. No. 1.08e-04;
Matches  11;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 6
ID   O14535           PRELIMINARY;      PRT;   113 AA.
AC   O14535;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED).
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   HRV FAB N6-VL (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PBL;
RA   ITOH K., SUZUKI T.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB006842; D1023041; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER        113       113
SQ   SEQUENCE   113 AA;  12207 MW;  A546C704 CRC32;

Db   6 MTQSPSSLSAAS 16
       |||||||||:||
Qy  24 MTQSPSSLSAS 34

Query Match        96.8%;  Score 61;  DB 4;  Length 113;
Best Local Similarity  90.9%;  Pred. No. 3.94e-04;
Matches  10;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

RESULT 7
ID   Q15982           PRELIMINARY;      PRT;   116 AA.
AC   Q15982;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED).
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   RHEUMATOID FACTOR C6 LIGHT CHAIN (FRAGMENT).
GN   V<KAPPA>1.
```

OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   ERMEL R.W., KENNY T.P., CHEN P.P., ROBBINS D.L.;
RL   ARTHRITIS RHEUM. (MUNCH.) 36:380-388(1993).
DR   EMBL; S56182; G298561; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER   1   1
FT   NON_TER   116   116
SQ   SEQUENCE   116 AA;   12528 MW; BFFBD90D CRC32;

Db   4 MTQSPSTLSAS 14
             ||||||:||||
         24 MTQSPSLSAS   34

Query Match   Best Local Similarity   90.9%;
Matches   10;   Conservative   1;   Score 61;   DB 4;   Length 116;
Pred. No. 3.94e-04;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT   8
ID   O43690   PRELIMINARY;   PRT;   239 AA.
AC   O43690;
DT   01-JUN-1998 (TREMBLREL. 06, CREATED)
DT   01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   ANTI-MPL SCFV (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   GODDARD A., YUAN J., ZHU Z., CARTER P.;
RL   SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AF048775; G2911502; -.
FT   NON_TER   1   1
FT   NON_TER   239   239
SQ   SEQUENCE   239 AA;   25262 MW; 5B9ABF4C CRC32;

Db   136 MTQSPSTLSAS 146
             ||||||:||||
         24 MTQSPSLSAS   34

Query Match   Best Local Similarity   90.9%;
Matches   10;   Conservative   1;   Score 61;   DB 4;   Length 239;
Pred. No. 3.94e-04;   Mismatches   0;   Indels   0;   Gaps   0;

Matches   10;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;

Db   136 MTQSPSTLSAS 146
             ||||||:||||
Qy   24 MTQSPSLSAS   34

RESULT   9
ID   O80289   PRELIMINARY;   PRT;   240 AA.
AC   O00289;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   SINGLE-CHAIN FV FRAGMENT (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
GN   SCFV.
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KONTERMANN R.E., WING M.G., WINTER G.;
RL   NAT. BIOTECHNOL. 15:629-631(1997).
DR   EMBL; Y13056; E315281; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER   1   1
FT   NON_TER   240   240
SQ   SEQUENCE   240 AA;   25569 MW; 6472A9C9 CRC32;

Db   136 MTQSPSTLSAS 146
             ||||||:||||
         24 MTQSPSLSAS   34

Query Match   Best Local Similarity   90.9%;
Matches   10;   Conservative   1;   Score 61;   DB 4;   Length 240;
Pred. No. 3.94e-04;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT   10
ID   O00288   PRELIMINARY;   PRT;   244 AA.
AC   O00288;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   SINGLE-CHAIN FV FRAGMENT (FRAGMENT).
SCFV.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KONTERMANN R.E., WING M.G., WINTER G.;
RL   NAT. BIOTECHNOL. 15:629-631(1997).
DR   EMBL; Y13057; E315275; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER   1   1
FT   NON_TER   244   244
SQ   SEQUENCE   244 AA;   26127 MW; A4CF148B CRC32;

Db   140 MTQSPSTLSAS 150
             ||||||:||||
Qy   24 MTQSPSLSAS   34

Query Match   Best Local Similarity   90.9%;
Matches   10;   Conservative   1;   Score 61;   DB 4;   Length 244;
Pred. No. 3.94e-04;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT   11
ID   O43689   PRELIMINARY;   PRT;   244 AA.
AC   O43689;
DT   01-JUN-1998 (TREMBLREL. 06, CREATED)
DT   01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   ANTI-HER3 SCFV (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   GODDARD A., YUAN J., ZHU Z., CARTER P.;
RL   SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AF048774; G2911500; -.
FT   NON_TER   1   1
FT   NON_TER   244   244
SQ   SEQUENCE   244 AA;   26025 MW; 47670049 CRC32;

Db   141 MTQSPSTLSAS 151
             ||||||:||||
         24 MTQSPSLSAS   34

Query Match   Best Local Similarity   90.9%;
Matches   10;   Conservative   1;   Score 61;   DB 4;   Length 244;
Pred. No. 3.94e-04;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT   12
ID   O14540   PRELIMINARY;   PRT;   113 AA.
AC   O14540;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   HRV FAB 027-VL (FRAGMENT).
OS   HOMO SAPIENS (HUMAN).

```
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PBL;
RA   ITOH K., SUZUKI T.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AB006849; D1023047; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER       113    113
SQ   SEQUENCE   113 AA;  12383 MW;  FCEB1F02 CRC32;

          Query Match  95.2%;  Score 60;  DB 4;  Length 113;
          Best Local Similarity  90.9%;  Pred. No. 7.47e-04;
          Matches  10;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Db           6  MTQSPSSLPAS  16
                ||||||||:||
Query Match  24  MTQSPSSLSAS  34
```

```
RESULT 13
ID   P97771        PRELIMINARY;        PRT;   241 AA.
AC   P97771;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   ANTI-CEA 79 SINGLE CHAIN FV FRAGMENT (FRAGMENT).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   CHUNG J.H., LEE S.D., YI K.S., SUH P.G., RYU S.H., CHOI S.J., KIM H.J.,
RA   KIM I.J., CHOI I.H., CHUNG H.K.;
RL   SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U88067; G1850548; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER         1      1
FT   NON_TER       241    241
SQ   SEQUENCE   241 AA;  26086 MW;  EBB2D29D CRC32;

          Query Match  88.9%;  Score 56;  DB 11;  Length 241;
          Best Local Similarity  90.9%;  Pred. No. 9.20e-03;
          Matches  10;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Db         137  LTQSPSSLSAS  147
                :||||||||||
Query Match  24  MTQSPSSLSAS  34
```

```
RESULT 14
ID   Q99818        PRELIMINARY;        PRT;   108 AA.
AC   Q99818;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   ANTI-SSDNA ANTIBODY LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN   HUMKV328H5.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   SUENAGA R.;
RL   SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U82258; G1773057; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER         1      1
FT   NON_TER       108    108
SQ   SEQUENCE   108 AA;  11792 MW;  876D5BA3 CRC32;

          Query Match  87.3%;  Score 55;  DB 4;  Length 108;
          Best Local Similarity  72.7%;  Pred. No. 1.70e-02;
          Matches  8;  Conservative  2;  Mismatches  1;  Indels  0;  Gaps  0;

Db           4  MTQSPATLSVS  14
                ||||:||:||:|
Qy          24  MTQSPSSLSAS  34
```

```
RESULT 15
ID   P97408        PRELIMINARY;        PRT;   102 AA.
AC   P97408;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   TYPE II COLLAGEN ANTIBODY KAPPA LIGHT CHAIN VARIABLE REGION
DE   (FRAGMENT).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DBA/1LJ;
RX   MEDLINE; 97257994.
RA   ITO H.O., UEDA T., HASHIMOTO Y., IMOTO T., KOGA T.;
RL   CELL. MOL. LIFE SCI. 53:51-60(1997).
DR   EMBL; U69539; G1731667; -.
DR   PFAM; PF00047; 1g.
FT   NON_TER         1      1
FT   NON_TER       102    102
SQ   SEQUENCE   102 AA;  11093 MW;  D3B638CD CRC32;

          Query Match  85.7%;  Score 54;  DB 11;  Length 102;
          Best Local Similarity  81.8%;  Pred. No. 3.13e-02;
          Matches  9;  Conservative  2;  Mismatches  0;  Indels  0;  Gaps  0;

Db           4  LTQSPTSLSAS  14
                :||||:||:|||
Qy          24  MTQSPSSLSAS  34

Search completed: Tue Apr 20 14:03:20 1999
Job time : 37 secs.
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MPSRCH™

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 20 14:06:47 1999; MasPar time 2.56 Seconds
                                          44.217 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-836-455-1.1
Perfect Score: 62   (50-56) from trans.pep (2 of 3)
Sequence: 1 GINLHWL 7

Scoring table: PAM 150
                Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: a-geneseq32

                1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
                8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
                14:part14 15:part15 16:part16 17:part17 18:part18
                19:part19 20:part20 21:part21 22:part22 23:part23
                24:part24 25:part25 26:part26 27:part27 28:part28
                29:part29

Statistics: Mean 16.909; Variance 67.405; scale 0.251

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description	Pred. No.
1	62	100.0	145	25	W27119	Murine monoclonal ant	2.56e+01
2	50	80.6	1082	13	R55017	pRb2 retinoblastoma t	2.73e+02
3	48	77.4	20	29	W45546	N-acetylamino-alcohol	4.00e+02
4	48	77.4	338	1	R04101	Sequence encoding Iso	4.00e+02
5	48	77.4	338	2	R03733	Cephalosporium acreno	4.00e+02
6	48	77.4	339	3	P60508	Isopenicillin N synth	4.00e+02
7	48	77.4	622	24	W22212	Rat transferrin recep	4.00e+02
8	48	77.4	760	24	W22213	Human transferrin rec	4.00e+02
9	46	74.2	321	1	P81342	Polypeptide involved	5.83e+02
10	46	74.2	356	3	R04066	T.variabilis D-amino	5.83e+02
11	46	74.2	356	2	P70388	D-amino acid oxidase.	5.83e+02
12	46	74.2	593	10	R00916	Sequence of a CD26 fr	5.83e+02
13	46	74.2	593	10	R54614	Delta594-C CD26.	5.83e+02
14	46	74.2	642	28	W43411	Yeast acylcoenzyme A:	5.83e+02
15	46	74.2	642	28	W38418	Yeast acyl-coenzyme A	5.83e+02
16	46	74.2	739	10	R54613	Delta24-34 CD26.	5.83e+02
17	46	74.2	759	10	R54612	Delta3-9 CD26.	5.83e+02
18	46	74.2	766	8	R40909	Sequence encoded by h	5.83e+02
19	46	74.2	766	10	R54611	Native CD26.	5.83e+02
20	45	72.6	245	16	R81415	Hepatitis GB virus (H	7.02e+02
21	45	72.6	359	7	R34102	Bacterial delta-6-des	7.02e+02
22	45	72.6	359	18	R99456	Synechocystis delta-6	7.02e+02
23	45	72.6	525	28	W26737	Staphylococcus carnos	7.02e+02
24	45	72.6	647	4	R20813	B lymphocyte-specific	7.02e+02
25	45	72.6	647	18	R91440	Human CD22 antigen.	7.02e+02
26	45	72.6	847	7	R33419	CD22-beta.	7.02e+02
27	45	72.6	3164	16	R94346	Hepatitis GB virus (H	7.02e+02
28	45	72.6	67	22	W20485	H. pylori secreted or	8.45e+02
29	44	71.0	107	7	R38601	HYH light chain.	8.45e+02
30	44	71.0	109	18	R52033	Light chain variable	8.45e+02
31	44	71.0	160	21	W11791	Early onset Alzheimer	8.45e+02
32	44	71.0	218	21	R86811	Saccharomyces cerevis	8.45e+02
33	44	71.0	388	19	W04405	Mouse CRTAM.	8.45e+02
34	44	71.0	556	17	R77676	Rat Oct-1 protein.	8.45e+02
35	44	71.0	1451	5	R27819	CCVinsavc spike prote	8.45e+02
36	44	71.0	1453	5	R27820	CCV-C54 spike protein	8.45e+02
37	44	71.0	1454	9	R31038	E2 protein of Canine	8.45e+02
38	44	71.0	1454	9	R42468	Feline enteric corona	8.45e+02
39	44	71.0	1454	9	R42475	FECV/FIPV chimeric sp	8.45e+02
40	44	71.0	1454	9	R42472	FECV/FIPV chimeric sp	8.45e+02
41	44	71.0	1454	5	R24397	Prod. of the S gene o	8.45e+02
42	44	71.0	1454	5	R24511	Prod. of the S genome	8.45e+02
43	44	71.0	1483	15	P80474	Sequence of protein o	8.45e+02
44	44	71.0	1594	5	P81183	Sequence of the peplo	8.45e+02
45	44	71.0	1830	8	R44504	Urea amide lyase.	8.45e+02

ALIGNMENTS

```
RESULT 1

ID   W27119 standard; Protein; 145 AA.
AC   W27119;
DT   04-JAN-1998 (first entry)
DE   Murine monoclonal anti-idiotype antibody 11D10 VL region.
DE   Monoclonal antibody anti-idiotype antibody 11D10.
KW   Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
OS   human milk fat globule; HMFG; tumour; breast cancer; vaccine.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FH
FT   Peptide         1..20
FT                   /label= Sig_peptide
FT   Protein         21..145
FT                   /label= Mat_protein
FT   Region          21..43
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          109..117
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Region          118..127
FT                   /label= FR1
FT                   /note= "framework region 4"
PN   WO9722699-A2.
PD   26-JUN-1997.
PF   19-DEC-1996; U20757.
PR   13-DEC-1996; US-575762.
PR   19-DEC-1996; US-575762.
PR   20-DEC-1995; US-591965.
PA   26-JAN-1996; US-591965.
PA   (KENT ) UNIV KENTUCKY.
PI   Chatterjee M, Chatterjee SK, Foon KA;
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DR   WPI; 97-341690/31.
DR   N-PSDB; T85149.
PT   Monoclonal anti-idiotype antibody 11D10 - elicits immune response
PT   against human milk fat globule disease associated tumours,
PT   especially breast cancer
PS   Claim 9; Page 94; 130pp; English.
CC   This polypeptide sequence comprises the light chain variable region
CC   (VL) of monoclonal anti-idiotype antibody 11D10 produced by
CC   hybridoma cell line ATCC 12020.  11D10 was obtained by immunising
CC   naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype
CC   response.  It elicits an immune response against a specific epitope
CC   of a high mol.wt. mucin of human milk fat globule (HMFG).  It
CC   induces an immunological response to HMFG in mice, rabbits, monkeys
CC   and patients with advanced HMFG-associated tumours.  Pharmaceutical
CC   compositions and vaccines comprising 11D10, 11D10 polypeptides
CC   and/or 11D10 polynucleotides (see also T85149-50) are claimed.
CC   Also claimed are diagnostic kits and methods of using 11D10, 11D10
CC   polypeptides and/or 11D10 polynucleotides, including methods of
CC   treating HMFG-associated tumours. 11D10 is also used in a claimed
CC   method of palliating HMFG-associated disease and in claimed kits to
CC   detect or quantify anti-HMFG antibody.
SQ   Sequence 145 AA.

Query Match             100.0%;  Score 62;  DB 25;  Length 145;
Best Local Similarity   100.0%;
Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db          50 ginlhwl 56
               |||||||
Qy          50 GINLHWL 56


RESULT 2
ID   R65017 standard; Protein; 1082 AA.
AC   R65017;
DT   30-SEP-1995 (first entry)
DE   pRb2 retinoblastoma tumour suppressor protein.
KW   Retinoblastoma; tumour suppressor; pRb2; diagnostic.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   misc_difference 507..512
FT                   /note= "primer A (R65015) recognition site"

DR   WO9505470-A.
AC   R65017.
DT   23-FEB-1995.
PF   12-AUG-1994; U09293.
PR   12-AUG-1993; US-106493.
     (UTEM ) UNIV TEMPLE.
     Giordano A;
     WPI; 95-098768/13.
DR   N-PSDB; 082748.
PT   DNA encoding retinoblastoma suppressor protein, pRB2 - and
PT   recombinant cell lines, for the diagnosis and suppression of
PT   cells infected with adenovirus E1A.
PS   Claim 10; Page 19-22; 29pp; English.
CC   The retinoblastoma tumour suppressor protein, pRb2, binds to the
CC   E1A transforming domain, and is useful in the diagnosis of cells
CC   infected with adeno virus E1A or a related virus.  The protein
CC   may be administered as a cell growth suppressor to infected cells
CC   e.g. retinoblastoma interocular cancer cells, and may be useful
CC   for identifying other DNA tumour virus oncoproteins.
SQ   Sequence 1082 AA.

Query Match             80.6%;  Score 50;  DB 13;  Length 1082;
Best Local Similarity   71.4%;
Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Db          24 gndlhwl 30
               | :|||||
Qy          50 GINLHWL 56


RESULT 3
ID   W45546 standard; peptide; 20 AA.
AC   W45546;
DT   28-MAY-1998 (first entry)
DE   N-acetylamino-alcohol hydrolase N-terminal amino acid fragment.
KW   N-acetylamino-alcohol hydrolase; NAAH; cyclopentene; chiral;
KW   carbon source; N-terminus.
OS   Rhodococcus erythropolis.
PN   WO9745529-A1.
PN   04-DEC-1997.
PF   30-MAY-1997; E02838.
PR   18-APR-1997; CH-000908.
PR   30-MAY-1996; CH-001359.
PR   10-FEB-1997; CH-000282.
PA   (LONZ ) LONZA AG.
PI   Bernegger-egli C, Birch OM, Bossard P, Brieden W,
PI   Brux F, Burgdorf K, Duc L, Etter K, Guggisberg I,
PI   Sauter M, Urban EM;
DR   WPI; 98-032639/03.
PS   Claim 6; Page 54; 68pp; German.
PT   This is the specifically claimed N-terminal amino acid sequence of
PT   N-acetylamino-alcohol hydrolase from Rhodococcus erythropolis. The
PT   invention relates to microorganisms, or their enzymatic extracts, able
CC   to utilise cyclopentene derivatives as sole carbon (or carbon and
CC   nitrogen) source. The invention also relates to new N-acetylamino-alcohol
CC   hydrolases (NAAH) from the microorganisms for preparation of chiral
CC   1-amino-4-hydroxymethyl-2-cyclopentene from N-acyl precursors.
CC   Compared with other methods, this method of preparation involves fewer
CC   stages and does not require lithium aluminium hydride or other expensive
CC   reagents.
SQ   Sequence 20 AA;

Query Match             77.4%;  Score 48;  DB 29;  Length 20;
Best Local Similarity   100.0%;
Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Db           4 nlhwl 8
               |||||
Qy          52 NLHWL 56


RESULT 4
ID   R04101 standard; protein; 338 AA.
AC   R04101;
DT   10-SEP-1990 (first entry)
DE   Sequence encoding isopenicillin N synthetase activity
KW   Iso-penicillin N synthetase; Cephalosporin acremonium; antibiotic.
OS   Cephalosporin acremonium.
PN   AU8942347-A.
PN   11-JAN-1990.
PD   27-SEP-1989; -42347.
PF   01-JAN-1986; AU-042347.
PA   (ELIL) Eli Lilly and Co.
PI   Ingolia TD, Queener SH, Samson SM, Skatrud PL;
DR   N-PSDB; Q04021.
PT   WPI; 90-124616/17.
PT   Iso-penicillin N synthetase activating sequences isolated from DNA
PT   from Cephalosporin acremonium and used to increase antibiotic prodn.
PS   Disclosure; pp; English.
CC   This enzyme can be used to produce isopenicillin N from the tripeptide
CC   delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine. Isopenicillin N is a
CC   starting material for penicillin N and other cephalosporins. The greatest
CC   potential use of the enzyme is to condense other tripeptides into novel
CC   beta lactam derivatives.
CC   See also Q04022.
SQ   Sequence 338 AA.

Query Match             77.4%;  Score 48;  DB 1;  Length 338;
Best Local Similarity   57.1%;
Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Db         50 gvdlpwl 56
              |:||| ||
Qy         50 GINLHWL 56


RESULT 5
ID   R03733 standard; protein; 338 AA.
AC   R03733;
DT   24-JUL-1990 (first entry)
DE   Cephalosporium acremonium isopenicillin-N-synthetase.
KW   Isopenicillin-N-synthetase; enzyme.
OS   Cephalosporium acremonium.
PN   US485251-B.
PD   05-DEC-1989.
PF   08-AUG-1986; 895008.
PR   08-AUG-1986; US-895008.
PA   (ELLI) Eli Lilly & Co.
PI   Ingolia TD, Queener SW, Samson SM, Skatrud PL, Godfrey OW;
DR   WPI; 90-044769/06.
DR   N-PSDB; Q03261.
PT   New recombinant DNA compounds encoding-isopenicillin-N-synthetase -
PT   used to produce vectors for improving fermentation efficiency and
PT   yield of penicillin antibiotic-producing organisms, etc.
PS   Claim 4; Page 25; 40pp; English.
CC   The protein is encoded in plasmid pPS19 and plasmid pS24.
CC   It has been used to construct novel E. coli expression
CC   vectors that drive expression of a stable, active, and novel
CC   isopenicillin-N-synthetase in E. coli. See also Q03267.
SQ   Sequence  338 AA;

Query Match        77.4%;  Score 48;  DB 2;  Length 338;
Best Local Similarity   57.1%;
Matches     4;  Conservative   2;  Mismatches  1;  Indels  0;  Gaps  0;


Db         50 gvdlpwl 56
              |:||| ||
Qy         50 GINLHWL 56


RESULT 6
ID   P60508 standard; protein; 339 AA.
AC   P60508;
DT   24-MAY-1991 (first entry)
DE   Isopenicillin N synthetase.
KW   Isopenicillin N synthetase.
OS   Cephalosporium acremonium.
PN   AU865431-A.
PD   30-OCT-1986.
PF   21-APR-1986; 056431.
PR   22-APR-1985; US-725870.
PR   18-NOV-1985; US-799384.
PR   08-AUG-1986; US-895008.
PA   (ELLI ) ELI LILLY & CO.
PI   Ingolia TD, Queener SW, Samson SM, Skatrud PL;
WPI; 86-325839/50.
DR   N-PSDB; N60414.
PT   New DNA encoding iso-penicillin N synthetase - for use in vectors
PT   permitting high level expression, esp. in prodn. of penicillin
PT   and cephalosporin antibacterials
PS   Claim 28; Page 86-7; 113pp; English.
CC   Isopenicillin N synthetase (IPS) can be expressed using a vector
CC   which permits high level expression of IPS activity in E.coli. The
CC   IPS from E.coli forms isopenicillin N from delta-(L-alpha-aminoadipyl)
CC   -L-cysteinyl-D-valine, and is also useful for condensing other
CC   tripeptides to form new antibiotics.
SQ   Sequence  339 AA;

Query Match        77.4%;  Score 48;  DB 3;  Length 339;
Best Local Similarity   57.1%;
Matches     4;  Conservative   2;  Mismatches  1;  Indels  0;  Gaps  0;


Db         50 gvdlpwl 56
              |:||| ||
```


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Qy         50 GINLHWL 56


RESULT 7
ID   W22212 standard; protein; 622 AA.
AC   W22212;
DT   02-NOV-1997 (first entry)
DE   Rat transferrin receptor.
KW   Radiation; radiomimetic; exposure; transferrin receptor;
OS   Rattus norvegicus.
PN   WO9715830-A1.
PD   01-MAY-1997.
PF   21-OCT-1996; U16880.
PR   24-OCT-1995; US-547197.
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.
PI   Glomski CA, Gong JK;
DR   WPI; 97-259141/23.
PT   Detecting exposure to radiation or radio-mimetic agents - by
PT   correlation with a protein, such as transferrin receptor, present on
PT   the surface of red blood cells of a mammal
PS   Disclosure; Page 61-62; 83pp; English.
CC   This polypeptide comprises the rat transferrin receptor (TR).
CC   Claimed methods for detecting a mammal's prior exposure to
CC   radiation or radiomimetic agents (RAs) involve: isolating red blood
CC   cells from the mammal, and detecting the quantity of TRs on the red
CC   blood cells using e.g. an antibody raised against the TR. The
CC   quantity of TRs on the red blood cells is correlated with the
CC   mammal's prior exposure. It is possible to assess accurately
CC   cumulative lifetime exposure and to directly study the effects of
CC   low doses of radiation, e.g. on cancer risk and other delayed
CC   responses. The limited amount of blood necessary permits the test
CC   to be conducted as frequently as desired. The test's sensitivity,
CC   extending from 0.1 cGy to over 600 cGy, spans both the environmental
CC   and the lethal dose ranges.
SQ   Sequence  622 AA;

Query Match        77.4%;  Score 48;  DB 24;  Length 622;
Best Local Similarity   57.1%;
Matches     4;  Conservative   3;  Mismatches  0;  Indels  0;  Gaps  0;


Db         498 glslgwl 504
              |:||| ||
Qy         50 GINLHWL 56


RESULT 8
ID   W22213 standard; protein; 760 AA.
AC   W22213;
DT   02-NOV-1997 (first entry)
DE   Human transferrin receptor.
KW   Radiation; radiomimetic; exposure; transferrin receptor;
OS   Homo sapiens.
PN   WO9715830-A1.
PD   01-MAY-1997.
PF   21-OCT-1996; U16880.
PR   24-OCT-1995; US-547197.
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.
PI   Glomski CA, Gong JK;
DR   WPI; 97-259141/23.
PT   Detecting exposure to radiation or radio-mimetic agents - by
PT   correlation with a protein, such as transferrin receptor, present on
PT   the surface of red blood cells of a mammal
PS   Disclosure; Page 63-65; 83pp; English.
CC   This polypeptide comprises the human transferrin receptor (TR).
CC   Claimed methods for detecting a mammal's prior exposure to
CC   radiation or radiomimetic agents (RAs) involve: isolating red blood
CC   cells from the mammal, and detecting the quantity of TRs on the red
CC   blood cells using e.g. an antibody raised against the TR. The
CC   quantity of TRs on the red blood cells is correlated with the
CC   mammal's prior exposure. It is possible to assess accurately
CC   cumulative lifetime exposure and to directly study the effects of
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CC   low doses of radiation, e.g. on cancer-risk and other delayed
CC   responses. The limited amount of blood necessary permits the test
CC   to be conducted as frequently as desired. The test's sensitivity,
CC   extending from 0.1 cGy to over 600 cGy, spans both the environmental
CC   and the lethal dose ranges.
SQ   Sequence 760 AA;

Query Match    77.4%;   Score 48;  DB 24;  Length 760;
Best Local Similarity 77.4%;  Pred. No. 4.00e+02;
Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Db    636  glslqwl 642
             |:|:||:||
Qy     50  GINLHWL 56


RESULT 9
ID   P81342 standard; protein; 321 AA.
AC   P81342;
DT   19-OCT-1990 (first entry)
DE   Polypeptide involved in protective mechanisms
KW   Immune response; cell growth.
PN   J6303298-A.
PD   30-JAN-1988.
PF   16-JUL-1986; 167518.
PR   16-JUL-1986; JP-167518.
PA   (DAIN) Dainippon Pharm KK.
DR   WPI; 88-068419/10.
DR   P-PSDB; P81342.
PT   New Polypeptide and DNA encoding it - related to protective
PT   mechanisms such as immune response etc.
PS   Disclosure: P; Japanese.
CC   This Polypeptide is involved in protective mechanisms such as immune
CC   response, cell growth and activation of protective functions.
SQ   Sequence 321 AA;

Query Match    74.2%;   Score 46;  DB 1;  Length 321;
Best Local Similarity 74.2%;  Pred. No. 5.83e+02;
Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Db    133  gvdlawl 139
             |:||:||
Qy     50  GINLHWL 56


RESULT 10
ID   R04066 standard; Protein; 356 AA.
AC   R04066;
DT   03-SEP-1990 (first entry)
DE   T.variabilis D-amino acid oxidase gene product.
KW   D-amino acid oxidase; cephalosporin; cephem; E.coli.
OS   Trigonopsis variabilis.
PN   EP-364275-A.
PD   18-APR-1990.
PF   12-OCT-1989; 310483.
PR   13-OCT-1989; JP-260332.
PA   (FUJI) Fujisawa Pharm KK.
PI   Isogai T, Ono H, Kojo H;
DR   WPI; 90-117771/16.
PT   D-amino acid oxidase, prodn. -
PT   by culture of E.coli transformants contg. expression vectors
PT   originated from Fusarium solani M-0718.
PS   Disclosure; Fig 9; 38pp; English.
CC   E.coli transformed to express DAO, which catalyses the enzymatic
CC   conversion of cephalosporin C to 7-beta-(5-carboxy-5-
CC   oxopentanamido)cephalosporanic acid (keto-7ACA). 7ACA is an
CC   important starting point for the production of cephem
CC   antibiotics.
SQ   Sequence 356 AA;

Query Match    74.2%;   Score 46;  DB 3;  Length 356;
Best Local Similarity 74.2%;  Pred. No. 5.83e+02;
Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Db    149  gvylnwl 155
             |:|:||
Qy     50  GINLHWL 56


RESULT 11
ID   P70388 standard; protein; 356 AA.
AC   P70388;
DT   14-JAN-1991 (first entry)
DE   D-amino acid oxidase;
DE   D-amino acid oxidase; Trigonopsis variabilis; cephalosporin;
KW   oxidative deamination.
OS   Trigonopsis variabilis.
PN   J62626994-A.
PD   16-NOV-1987.
PF   12-MAY-1986; J06663.
PR   12-MAY-1986; JP-106663.
PA   (ASAH ) ASAHI CHEMICAL IND KK.
DR   WPI; 87-359677/51.
DR   N-PSDB; N70609.
PT   DNA fragment encoding D-amino acid oxidase - which is a useful
PT   enzyme for the catalytic oxidative deamination of D-amino acids.
PS   Claim 1; Page 583-4; 12pp; Japanese.
CC   D-amino acid oxidase catalyses the oxidative deamination of D-amino
CC   acids. It is used in the prepn. of L-amino acids from racemates,
CC   in the prepn. of ketoic acid from D-amino acid, in amino acid
CC   analysis, etc. The enzyme can oxidise cephalosporin C to
CC   7-beta-(5-carboxy-5-oxopentanamide)cephalosporanic acid, which
CC   reacts with hydrogen peroxide to give 7-beta-(4-carboxybutanamide)-
CC   cephalosporanic acid. These cpds. are important intermediates for
CC   synthesis of cephalosporin type antibiotics.
SQ   Sequence 356 AA;

Query Match    74.2%;   Score 46;  DB 2;  Length 356;
Best Local Similarity 74.2%;  Pred. No. 5.83e+02;
Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Db    149  gvylnwl 155
             |:|:||
Qy     50  GINLHWL 56


RESULT 12
ID   R40916 standard; Protein; 593 AA.
AC   R40916;
DT   05-FEB-1994 (first entry)
DE   Sequence of a CD26 fragment lacking a portion of the carboxy
DE   terminal region
KW   Human T cell activation antigen; monoclonal antibody Ta1; CD26.
OS   Synthetic.
PN   W09316102-A.
PD   19-AUG-1993.
PF   09-APR-1992; U02892.
PR   06-FEB-1992; US-832211.
PA   (DAND ) DANA FARBER CANCER INST INC.
PI   Morimoto C, Schlossman SF, Tanaka T;
DR   WPI; 93-272827/34.
PT   Polypeptide fragments of CD26 - are capable of disrupting binding
PT   of CD45 and CD26 and thus interfering with T-cell activation
PS   Example; Pages 46-48; 73pp; English.
CC   C26 is a human T cell antivation antigen originally identified by
CC   its reactivity with the MAb Ta1. C26 cDNA library was constructed
CC   from human PHA-activated T cells using the CDM7 vector.
CC   Fragments of CD26 can be prepd in the following manner.
CC   CD26 XbaI-SphI cDNA fragment is ligated to the vector
CC   RcSR-alpha-26 XbaI-HindIII DNA fragment and the linker 046092.
CC   The linker introduces an in-frame stop codon that results in the
CC   deletion of the segment of CD26 from AA 594 to the carboxy
CC   terminus of the wild-type protein. This deletion mutant, shown
CC   in R40916, lacks the putative catalytic site of CD26 and has a new
CC   carboxy terminus given in R40917.
SQ   Sequence 593 AA;

Query Match    57.1%;   Score 46;  DB 3;  Length 356;
Best Local Similarity 57.1%;  Pred. No. 5.83e+02;
Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Query Match                    74.2%;   Score 46; DB 8; Length 593;
Best Local Similarity  66.7%;  Pred. No. 5.83e+02;
Matches      4; Conservative  2; Mismatches  0; Indels  0; Gaps  0;

Qy  51 INLHWL 56

Db  311 lslqwl 316
```

```
RESULT  13

ID   R54614 standard; Protein; 593 AA.
AC   R54614;
DT   09-DEC-1994 (first entry)
DE   Delta594-C CD26.
KW   Human; T cell activation antigen; CD26; analogues; deletion; soluble;
KW   signal peptidase; immune-stimulating; response-stimulating; AIDS;
KW   immunosuppression; AIDS-related complex.
OS   Homo sapiens.
     Key                Location/Qualifiers
FT   misc_difference    593
FT                      /note= "Position of delta594-C deletion"
PN   WO9409132-A.
PD   28-APR-1994.
PD   19-AUG-1993;
PR   21-AUG-1992;  US-934162.
PA   (DAND ) DANA FARBER CANCER INST INC.
PI   Morimoto C, Schlossman S, Tanaka T;
DR   WPI; 94-151317/18.
PT   Polypeptide fragments and analogues of CD26 and encoding nucleic
PT   acid - useful for stimulating immune response, e.g. for treatment
PT   of AIDS, to counteract immunosuppressive drug, and as vaccine
PT   adjuvant.
PS   Disclosure; Page 56-58; 85pp; English.
CC   The sequences given in R54612-14 represents analogues of the human T
CC   cell activation antigen CD26 which have internal deletions. The
CC   analogues pref. lack residues 3-9 or 24-34. These analogues are
CC   soluble under physiological conditions and lack enough amino acid
CC   residues to render them susceptible to cleavage by signal peptidase.
CC   The peptide fragments and analogues are useful as immune or response-
CC   stimulating therapeutics, eg, they may be used for treatment of
CC   disease conditions characterised by immunosuppression, eg. AIDS or
CC   AIDS-related complex, other virally or environmentally-induced
CC   conditions, and certain congenital immune deficiencies. The peptides
CC   can be employed to increase immune function which has been impaired by
CC   use of immunosuppressive drugs, such as certain chemotherapeutic drugs.
SQ   Sequence  593 AA;
```

```
Query Match                    74.2%;   Score 46; DB 10; Length 593;
Best Local Similarity  66.7%;  Pred. No. 5.83e+02;
Matches      4; Conservative  2; Mismatches  0; Indels  0; Gaps  0;

Qy  51 INLHWL 56

Db  311 lslqwl 316
```

```
RESULT  14

ID   W43411 standard; Protein; 642 AA.
AC   W43411;
DT   08-JUN-1998 (first entry)
DE   Yeast acylcoenzyme A:cholesterol acyltransferase-related enzyme II.
KW   Acylcoenzyme A:cholesterol acyltransferase; ACAT II;
KW   ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;
KW   inhibitor; atherosclerosis; hyperlipidaemia; yeast.
OS   Saccharomyces cerevisiae.
     Key                Location/Qualifiers
FH   Domain             215..231
FT                      /note= "transmembrane domain"
FT   Domain             439..451
FT                      /note= "transmembrane domain"
PN   WO9745439-A1.
PD   04-DEC-1997.
```

```
PF   30-MAY-1997; U09460.
PR   30-MAY-1996; US-657620.
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
PI   Sturley SL;
DR   WPI; 98-032573/03.
DR   N-PSDB; V01538.
PT   DNA encoding acylcoenzyme A: cholesterol acyltransferase II or
III  - useful to identify inhibitors for treatment of
PT   atherosclerosis or hyperlipidaemia
CC   This protein comprises yeast acylcoenzyme A:cholesterol
CC   acyltransferase-related enzyme II. The invention relates to
CC   isolated nucleic acids (see VO1533-35) coding for human and mouse
CC   acylcoenzyme A:cholesterol acyltransferase II and III (see
CC   W43406-08), also designated ACAT related gene products (ARGP) 1
CC   and 2. These can be used to identify inhibitors useful in the
CC   treatment of atherosclerosis and hyperlipidaemia.
SQ   Sequence  642 AA;
```

```
Query Match                    74.2%;   Score 46; DB 29; Length 642;
Best Local Similarity  66.7%;  Pred. No. 5.83e+02;
Matches      4; Conservative  2; Mismatches  0; Indels  0; Gaps  0;

Qy  51 INLHWL 56

Db  316 lklhwl 321
```

```
RESULT  15

ID   W38418 standard; Protein; 642 AA.
AC   W38418;
DT   21-MAY-1998 (first entry)
DE   Yeast acyl-coenzyme A:cholesterol acyltransferase 2.
KW   Acyl-coenzyme A: cholesterol acyltransferase 2; ARE2; yeast;
KW   sterol; esterification; arteriosclerosis; hyperlipidaemia;
KW   antifungal; fungicide.
OS   Saccharomyces cerevisiae.
     Key                Location/Qualifiers
FH   Domain             215..231
FT                      /note= "putative transmembrane domain"
FT   Domain             439..451
FT                      /note= "putative transmembrane domain"
PN   WO9745536-A1.
PD   04-DEC-1997.
PF   30-MAY-1997; U09160.
PR   30-MAY-1996; US-657621.
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
PI   (INDV ) UNIV INDIANA FOUND.
PI   Bard M, Sturley SL, Yang H;
DR   WPI; 98-032644/03.
DR   N-PSD; T96370.
PT   Yeast acyl:coenzyme A:transferase related enzyme I
and II - useful to identify inhibitor for treatment of
PT   hyperlipidaemia, arteriosclerosis and fungal invasion
PS   Example 1; Page 71-73; 111pp; English.
CC   Yeast acyl-coenzyme A:cholesterol acyltransferase 2 (ARE2) is
CC   encoded by a gene (see T96370) located on chromosome X or XIV that
CC   was identified by homology to the human acyl-coenzyme A:cholesterol
CC   acyltransferase 1 gene (see T96368). ARE2 and ARE1 (see W38417)
CC   exhibit significant structural and functional homology to the
CC   putative catalytic component of cholesterol esterification in
CC   human macrophages. A consensus sequence of the yeast and human
CC   proteins is given in W38419. Deletion of the ARE1 and ARE2 genes
CC   produces a viable yeast cell with undetectable esterified sterol.
CC   A claimed expression vector comprises a nucleic acid molecule
CC   encoding yeast wild type ARE1 or ARE2 operatively linked to a
CC   promoter of RNA transcription. The vector and a claimed
CC   host-vector system can be used for the recombinant production of
CC   ARE1 or ARE2. The products can be used to identify novel ARE1 or
CC   ARE2 inhibitors. ARE2 inhibitors can be used to treat
CC   arteriosclerosis or hyperlipidaemia. ARE1 and ARE2 inhibitors can
CC   also be used to inhibit fungal growth or to treat fungal invasion
CC   (all claimed).
```

SQ   Sequence   642 AA;   ---

      Query Match   74.2%;   Score 46;   DB 28;   Length 642;
      Best Local Similarity 66.7%;   Pred. No. 5.83e+02;
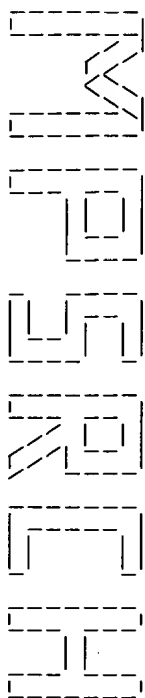   Matches   4; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Db   316 1klhwl 321
         : :|:|||
Qy   51 INLHWL 56

Search completed: Tue Apr 20 14:07:03 1999
Job time : 16 secs.

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**          M P S R C H  (TM)                  **
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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 20 14:06:10 1999; MasPar time 3.12 Seconds
                                 84.038 Million cell updates/sec

Tabular output not generated.

Title:	
Description:	>US-08-836-455-1_1
	(50-56) from trans.pep (2 of 3)
Perfect Score:	62
Sequence:	1 GINLHWL 7
Scoring table:	PAM 150
	Gap 11
Searched:	116695 seqs, 37453910 residues
Post-processing:	Minimum Match 0%
	Listing first 45 summaries
Database:	PirS8
	1:pir1 2:pir2 3:pir3 4:pir4
Statistics:	Mean 23.536; Variance 40.703; scale 0.578

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	58	93.5	964	2	E70826	probable membrane pro	3.77e+00
2	53	85.5	712	2	S64828	SSK1 protein - yeast	2.29e+01
3	53	85.5	967	2	C70831	probable mmpl4 protei	2.29e+01
4	52	83.9	459	2	S10196	NADH dehydrogenase (u	3.25e+01
5	51	82.3	495	2	S75895	hypothetical protein	4.60e+01
6	50	80.6	316	2	B71301	probable tRNA delta(2	6.47e+01
7	50	80.6	372	2	B70661	hypothetical protein	6.47e+01
8	50	80.6	476	2	A70477	hypothetical protein	6.47e+01
9	50	80.6	687	2	B64126	glutamate synthase sm	6.47e+01
10	50	80.6	791	2	D64629	transposase homolog H	6.47e+01
11	50	80.6	811	2	S04085	iron-regulated outer	6.47e+01
12	50	80.6	811	2	A33829	ovarian tumor locus P	6.47e+01
13	50	80.6	1082	2	I38150	ovarian tumor protein	6.47e+01
14	50	80.6	1139	2	A49370	Rb2/p130 protein - hu	6.47e+01
15	50	80.6	1139	2	A49369	E1A-associated cyclin	6.47e+01
16	49	79.0	192	2	S09533	adenovirus E1A-associ	9.06e+01
17	49	79.0	214	2	B40296	CI protein - phage 18	9.06e+01
18	49	79.0	322	2	S60783	hypothetical protein	9.06e+01
19	49	79.0	305	2	S75279	lipopolysaccharide he	9.06e+01
20	48	77.4	205	2	A71177	hypothetical protein	1.26e+02
21	48	77.4	306	2	B36263	probable thymidylate	1.26e+02
22	48	77.4	338	2	S09312	oligopeptide transpor	1.26e+02
23	48	77.4	338	2	A24567	isopenicillin N synth	1.26e+02
24	48	77.4	348	2	B33604	isopenicillin N synth	1.26e+02
25	48	77.4	379	2	JC4843	rfbE protein - Salmon	1.26e+02
26	48	77.4	476	1	WZEC	ATP-gated ionchannel	1.26e+02
27	48	77.4	502	2	S41544	tryptophanase (EC 4.1	1.26e+02
28	48	77.4	522	2	A34549	vsrA protein - Pseudo	1.26e+02
29	48	77.4	757	2	A48592	transferrin receptor	1.26e+02
30	48	77.4	760	2	JXHU	transferrin receptor	1.26e+02
31	48	77.4	763	2	S29548	transferrin receptor	1.26e+02
32	48	77.4	810	2	S43156	transferrin receptor	1.26e+02
33	48	77.4	810	1	G01252	small GTP binding pro	1.26e+02
34	48	77.4	859	2	A64742	hypothetical protein	1.26e+02
35	48	77.4	964	2	A32713	reverse transcriptase	1.26e+02
36	48	77.4	964	2	S13329	hypothetical protein	1.26e+02
37	47	75.8	141	2	S73543	MG427 homolog C12_orf	1.75e+02
38	47	75.8	348	2	A70311	hypothetical protein	1.75e+02
39	47	75.8	410	2	S56562	hypothetical 44.7K pr	1.75e+02
40	47	75.8	417	2	JW0068	triacylglycerol lipas	1.75e+02
41	47	75.8	901	2	S50987	SOK1 protein - yeast	1.75e+02
42	46	74.2	302	1	QREBOB	sss protein - Pseudom	2.42e+02
43	46	74.2	306	1	QREBOB	oligopeptide permease	2.42e+02
44	46	74.2	495	2	S06740	envelope protein E (v	2.42e+02
45	46	74.2	642	2	S63350	probable membrane pro	2.42e+02
```

ALIGNMENTS

```
RESULT          1
ENTRY           E70826         #type complete
TITLE           probable membrane protein - Mycobacterium tuberculosis
                 (strain H37RV)
ORGANISM        #formal_name Mycobacterium tuberculosis
DATE            17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                17-Jul-1998
ACCESSIONS      E70826
REFERENCE       A70500
  #authors      Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
                C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry
                III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.;
                Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
                Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
                Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
                Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
                Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
                Skelton, S.; Squares, S.; Sqares, R.; Sulston, J.E.;
                Taylor, K.; Whitehead, S.; Barrell, B.G.
  #journal      Nature (1998) 393:537-544
  #title        Deciphering the biology of Mycobacterium tuberculosis from
                the complete genome sequence.
  #cross-references MUID:98295987
  #accession    E70826
    #molecule_type DNA
    #residues   1-964 #label COL
    #cross-references GB:AL021943; GB:AL123456; NID:g3261530; PID:e1253102;
                      PID:g2909649
    #experimental_source strain H37Rv
GENETICS
    #gene       mmpL5
SUMMARY         #length 964 #molecular-weight 104784 #checksum 7944

Query Match     93.5%;  Score 58;  DB 2;  Length 964;
Best Local Similarity  85.7%;
Matches    6;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Qy         50 GINLHWL 56
              ||:||||
Db        828 GIELHWL 834


RESULT          2
ENTRY           S64828         #type complete
TITLE           SSK1 protein - yeast (Saccharomyces cerevisiae)
```

ALTERNATE_NAMES protein L1539; protein YLR006c
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 01-Aug-1995 #sequence_revision 24-May-1996 #text_change
06-Feb-1998
ACCESSIONS S64742
REFERENCE S64828; S45308
#authors Vandenbol, M.; Portetelle, D.; Hilger, F.
#submission submitted to the Protein Sequence Database, May 1996
#accession S64828
#molecule_type DNA
#residues 1-712 ##label VAN
##cross-references EMBL:Z73178; NID:g1360295; PID:e245767; PID:g1360296;
MIPS:YLR006c
REFERENCE S45308
#authors Maeda, T.; Wurgler-Murphy, S.M.; Saito, H.
#journal Nature (1994) 369:242-245
#title A two-component system that regulates an osmosensing MAP
kinase cascade in yeast.
#accession S45308
##status nucleic acid sequence not shown; not compared with
conceptual translation
GENETICS #map_position 12R
#gene SGD:SSK1
##cross-references SGD:S0003996; MIPS:YLR006c
FUNCTION #description signal transduction
CLASSIFICATION #superfamily response regulator homology
KEYWORDS phosphoprotein; signal transduction; two-component regulatory
system
FEATURE 506-613 #domain response regulator homology #label RRH\
554 #binding_site phosphate (Asp) (covalent) #status
Predicted
SUMMARY #length 712 #molecular-weight 78529 #checksum 1343

Query Match
Best Local Similarity 83.3%; Score 53; DB 2; Length 712;
Matches 5; Conservative 1; Pred. No. 2.29e+01; Mismatches 0; Indels 0; Gaps 0;

Db 634 VNLHWL 639
        :|||||
Qy 51 INLHWL 56

RESULT 3
ENTRY C70831 #type complete
TITLE probable mmpl4 protein - Mycobacterium tuberculosis (strain
H37RV)
#formal_name Mmpl4 protein
ORGANISM Mycobacterium tuberculosis
DATE 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
ACCESSIONS C70831
REFERENCE C70831
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry
III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.;
Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
Skelton, S.; Squares, S.; Squares, R.; Sulston, J.E.;
Taylor, K.; Whitehead, S.; Barrell, B.G.
#journal Nature (1998) 393:537-544
#title Deciphering the biology of Mycobacterium tuberculosis from
the complete genome sequence.
##cross-references MUID:9825987
#accession C70831
##status preliminary; nucleic acid sequence not shown;

SUMMARY translation not shown
##molecule_type DNA
##residues 1-967 ##label COL
##cross-references GB:AL021932; GB:AL123456; NID:g3261527; PID:e1252519;
PID:g2909525
GENETICS #gene mmpl4
##experimental_source strain H37Rv
SUMMARY #length 967 #molecular-weight 105233 #checksum 3274

Query Match
Best Local Similarity 85.5%; Score 53; DB 2; Length 967;
Matches 5; Conservative 2; Pred. No. 2.29e+01; Mismatches 0; Indels 0; Gaps 0;

Db 823 AIHLHWL 829
        :|:||:||
Qy 50 GINLHWL 56

RESULT 4
ENTRY S10196 #type complete
TITLE NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 -
chicken mitochondrion (SGC1)
ORGANISM #formal_name mitochondrion Gallus gallus #common_name chicken
DATE 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change
08-Sep-1997.
ACCESSIONS S10196
REFERENCE S10196
S10187
#authors Desjardins, P.; Morais, R.
#journal J. Mol. Biol. (1990) 212:599-634
#title Sequence and gene organization of the chicken mitochondrial
genome. A novel gene order in higher vertebrates.
#cross-references MUID:90230301
#accession S10196
##molecule_type DNA
##residues 1-459 ##label DES
##cross-references EMBL:X52392; NID:g12960; PID:g12970
GENETICS #gene ND4
#genome mitochondrion
#genetic_code SGC1
CLASSIFICATION #superfamily NADH dehydrogenase (ubiquinone) chain 4
KEYWORDS membrane-associated complex; mitochondrion; NAD; oxidative
phosphorylation; oxidoreductase; respiratory chain
SUMMARY #length 459 #molecular-weight 51145 #checksum 1806

Query Match
Best Local Similarity 83.9%; Score 52; DB 2; Length 459;
Matches 5; Conservative 2; Pred. No. 3.25e+01; Mismatches 0; Indels 0; Gaps 0;

Db 36 SISLHWL 42
       :|:||||
Qy 50 GINLHWL 56

RESULT 5
ENTRY S75895 #type complete
TITLE hypothetical protein - Synechocystis sp. (strain PCC 6803)
ORGANISM #formal_name Synechocystis sp.
#variety PCC 6803
DATE 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
21-Aug-1998
ACCESSIONS S75895
REFERENCE S74322
S75895
#authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo,
S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Yasuda, M.; Tabata, S.
#journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular
cyanobacterium Synechocystis sp. PCC 6803. II. Sequence

Query Match
Best Local Similarity 71.4%; Score 52; DB 2; Length 459;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 36 SISLHWL 42
       :|:||||
Qy 50 GINLHWL 56

determination of the entire genome and assignment of
potential protein-coding regions.
#cross-references MUID:97061201
#accession S75895
##status   preliminary
##molecule_type DNA
##residues   1-495 ##label KAN
##cross-references EMBL:D90913; GB:AB001339; NID:g1653348; PID:d1019087;
             PID:g1653440
##note   the nucleotide sequence was submitted to the EMBL Data
             Library, June 1996
CLASSIFICATION #superfamily xylulokinase
SUMMARY   #length 495 #molecular-weight 54351 #checksum 4379

Query Match   82.3%; Score 51; DB 2; Length 495;
Best Local Similarity 71.4%; Pred. No. 4.60e+01;
Matches   5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 141 GTKLHWL 147
        | :||||
Qy   50 GINLHWL 56

RESULT 6
ENTRY   B71301   #type complete
TITLE   probable tRNA delta(2)-isopentenylpyrophosphate transferase
             (miaA) - syphilis spirochete
ORGANISM   #formal_name Treponema pallidum subsp. pallidum #common_name
             syphilis spirochete
DATE   24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change
             07-Aug-1998
ACCESSIONS   B71301
REFERENCE   A71250
#authors   Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.;
             Sutton, G.G.; Dodson, R.; Gwinn, M.; Hickey, E.K.; Clayton,
             R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod,
             M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson,
             D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDonald,
             L.; Artiach, P.; Bowman, C.; Cotton, M.D.; Fujii, C.;
             Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Watthey,
             L.; Weidman, J.; Smith, H.O.; Venter, J.C.
#journal   Science (1998) 281:375-388
#title   Complete genome sequence of Treponema pallidum, the syphilis
             spirochete.
#accession   B71301
##status   preliminary; nucleic acid sequence not shown;
##molecule_type DNA
##residues   1-316 ##label COL
##cross-references GB:AE001238; GB:AE000520; NID:g3322928; PID:g3322935
##experimental_source strain Nichols
GENETICS
#gene   TP0637
SUMMARY   #length 316 #molecular-weight 36174 #checksum 2660

Query Match   80.6%; Score 50; DB 2; Length 316;
Best Local Similarity 57.1%; Pred. No. 6.47e+01;
Matches   4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 300 GVKIHWL 306
        |:::|||
Qy   50 GINLHWL 56

RESULT 7
ENTRY   B70661   #type complete
TITLE   hypothetical protein Rv2337c - Mycobacterium tuberculosis
             (strain H37RV)
ORGANISM   #formal_name Mycobacterium tuberculosis
DATE   17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
ACCESSIONS   B70661
REFERENCE   A70500
#authors   Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
             C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry
             III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.;
             Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
             Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
             Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
             Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
             Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.;
             Skelton, S.; Squares, S.; Squares, R.; Sulston, J.E.;
             Taylor, K.; Whitehead, S.; Barrell, B.G.
#journal   Nature (1998) 393:537-544
#title   Deciphering the biology of Mycobacterium tuberculosis from
             the complete genome sequence.
#accession   B70661
##status   preliminary; nucleic acid sequence not shown;
##molecule_type DNA
##residues   1-372 ##label COL
##cross-references GB:Z83860; GB:AL123456; NID:g3261681; PID:e290744;
##experimental_source strain H37Rv
GENETICS
#gene   Rv2337c
SUMMARY   #length 372 #molecular-weight 41272 #checksum 8278

Query Match   80.6%; Score 50; DB 2; Length 372;
Best Local Similarity 71.4%; Pred. No. 6.47e+01;
Matches   5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 154 GIQLHWF 160
        ||:|||:
Qy   50 GINLHWL 56

RESULT 8
ENTRY   A70477   #type complete
TITLE   glutamate synthase small subunit gltD - Aquifex aeolicus
ORGANISM   #formal_name Aquifex aeolicus
DATE   08-May-1998 #sequence_revision 08-May-1998 #text_change
             13-Sep-1998
ACCESSIONS   A70477
REFERENCE   A70300
#authors   Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
             Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
             Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
             J.M.; Olson, G.J.; Swanson, R.V.
#journal   Nature (1998) 392:353-358
#title   The complete genome of the hyperthermophilic bacterium
             Aquifex aeolicus.
#accession   A70477
##status   preliminary; nucleic acid sequence not shown;
##molecule_type DNA
##residues   1-476 ##label AQF
##cross-references GB:AE000770; NID:g2984274; PID:g2984275; GB:AE000657
##experimental_source strain VF5
GENETICS
#gene   gltD
SUMMARY   #length 476 #molecular-weight 52947 #checksum 4062
CLASSIFICATION #superfamily glutamate synthase small chain

Query Match   80.6%; Score 50; DB 2; Length 476;
Best Local Similarity 57.1%; Pred. No. 6.47e+01;
Matches   4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 342 GVKIHWL 348
        |:::|||
Qy   50 GINLHWL 56

RESULT 9

ENTRY   B64126   #type complete
TITLE   transposase homolog H11478 - Haemophilus influenzae (strain
               Rd KW20)
ORGANISM   #formal_name Haemophilus influenzae
DATE   18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change
               24-Oct-1997
ACCESSIONS   B64126
REFERENCE   A64000
#authors   Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
               Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;
               Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
               Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
               Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
               J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
               M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Saudek,
               D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
               J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
               Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
#journal   Science (1995) 269:496-512
#title   Whole-genome random sequencing and assembly of Haemophilus
               influenzae Rd.
#cross-references MUID:95350630
##accession   B64126
##status   nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues   1-687 ##label TIGR
##cross-references GB:U32825; GB:L42023; NID:g1574307; PID:g1574318;
               TIGR:H11478
SUMMARY   #length 687   #molecular-weight 78719 #checksum 2570

Query Match   80.6%;   Score 50;   DB 2;   Length 687;
Best Local Similarity 83.3%;   Pred. No. 6.47e+01;
Matches   5; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Db 379 GIELHW 384
         |:||:||
Qy   50 GINLHW 55

RESULT   10

ENTRY   D64629   #type complete
TITLE   iron-regulated outer membrane protein - Helicobacter pylori
               (strain 26695)
ORGANISM   #formal_name Helicobacter pylori
DATE   09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change
               18-Sep-1998
ACCESSIONS   D64629
REFERENCE   A64520
#authors   Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
               Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
               H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
               J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
               Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
               McKenney, K.; Fitzegerald, L.M.; Lee, N.; Adams, M.D.;
               Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback, T.R.;
               Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
               Fujii, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
               W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser,
               C.M.; Venter, J.C.
#journal   Nature (1997) 388:539-547
#title   The complete genome sequence of the gastric pathogen
               Helicobacter pylori.
#cross-references MUID:97394467
##accession   D64629
##status   preliminary; nucleic acid sequence not shown;
               translation not shown
##molecule_type DNA
##residues   1-791 ##label TOM
##cross-references GB:AE000597; GB:AE000511; NID:g2314007; PID:g2314011;
               TIGR:HP0876
SUMMARY   #superfamily iron-regulated outer membrane protein
               #length 791 #molecular-weight 88525 #checksum 366

Query Match   80.6%;   Score 50;   DB 2;   Length 791;
Best Local Similarity 85.7%;   Pred. No. 6.47e+01;
Matches   6; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Db 665 GINLAWL 671
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Qy   50 GINLHWL 56

RESULT   11

ENTRY   S04085   #type complete
TITLE   ovarian tumor locus protein - fruit fly (Drosophila
               melanogaster)
ORGANISM   #formal_name Drosophila melanogaster
DATE   07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
               24-Sep-1998
ACCESSIONS   S04085
REFERENCE   S04085
#authors   Champe, M.A.; Laird, C.D.
#journal   Nucleic Acids Res. (1989) 17:3304
#title   Nucleotide sequence of a cDNA from the putative ovarian tumor
               locus of Drosophila melanogaster.
#cross-references MUID:89263747
##accession   S04085
##status   translation not shown
##molecule_type mRNA
##residues   1-811 ##label CHA
##cross-references EMBL:X13693; NID:g8315; PID:g8316
GENETICS
#gene   otu
##cross-references FlyBase:FBgn0003023
#map_position X
SUMMARY   #length 811   #molecular-weight 92616   #checksum 7288

Query Match   80.6%;   Score 50;   DB 2;   Length 811;
Best Local Similarity 66.7%;   Pred. No. 6.47e+01;
Matches   4; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Db 593 GVDLHW 598
         |:||:||
Qy   50 GINLHW 55

RESULT   12

ENTRY   A33829   #type complete
TITLE   ovarian tumor protein - fruit fly (Drosophila melanogaster)
ORGANISM   #formal_name Drosophila melanogaster
DATE   23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change
               24-Sep-1998
ACCESSIONS   A33829
REFERENCE   A33829
#authors   Steinhauer, W.R.; Walsh, R.C.; Kalfayan, L.J.
#journal   Mol. Cell. Biol. (1989) 9:5726-5732
#title   Sequence and structure of the Drosophila melanogaster
               ovarian tumor gene and generation of an antibody specific for the
               ovarian tumor protein.
#cross-references MUID:90066528
##accession   A33829
##status   preliminary
##molecule_type DNA; mRNA
##residues   1-811 ##label STE
##cross-references GB:M30825; NID:g158028; PID:g158029
GENETICS
#gene   FlyBase:otu
##cross-references FlyBase:FBgn0003023
SUMMARY   #length 811 #molecular-weight 92612 #checksum 7006

Query Match   80.6%;   Score 50;   DB 2;   Length 811;
Best Local Similarity 66.7%;   Pred. No. 6.47e+01;
Matches   4; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Db 593 GVDLHW 598
         |:||:||

Qy 50 GINLHW 55

RESULT 13
ENTRY   I38150   #type complete
TITLE   Rb2/p130 protein - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change
            29-Aug-1997
ACCESSIONS I38150; S36648
REFERENCE   I38150
  #authors Mayol, X.; Grana, X.; Baldi, A.; Sang, N.; Hu, Q.; Giordano,
            A.
  #journal Oncogene (1993) 8:2561-2566
  #title   Cloning of a new member of the retinoblastoma gene family
            (pRb2) which binds to the E1A transforming domain.
  #cross-references MUID:93368960
  #accession I38150
    ##status preliminary; translated from GB/EMBL/DDBJ
    ##molecule_type mRNA
    ##residues 1-1082 ##label RES
    ##cross-references EMBL:X74594; NID:g397147; PID:g397148
GENETICS
  #gene   GDB:RBL2
    ##cross-references GDB:269890; OMIM:180203
  #map_position 16q12.2-16q12.2
CLASSIFICATION #superfamily retinoblastoma-associated protein
SUMMARY   #length 1082 #molecular-weight 122475 #checksum 2127

Query Match   80.6%; Score 50; DB 2; Length 1082;
Best Local Similarity   71.4%;
Matches   5; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy 50 GINLHWL 56
       |:||||
Db 24 GNDLHWL 30

Qy 50 GINLHWL 56

RESULT 14
ENTRY   A49370   #type complete.
TITLE   E1A-associated cyclin-binding protein p130 - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change
            20-Mar-1998
ACCESSIONS A49370
REFERENCE   A49370
  #authors Hannon, G.J.; Demetrick, D.; Beach, D.
  #journal Genes Dev. (1993) 7:2378-2391
  #title   Isolation of the Rb-related p130 through its interaction with
            CDK2 and cyclins.
  #cross-references MUID:94074896
  #accession A49370
    ##status preliminary
    ##molecule_type mRNA
    ##residues 1-1139 ##label HAN
    ##cross-references GB:S67171; NID:g453131; PID:g453132
    ##experimental_source HeLa S3 suspension cells
    ##note   sequence extracted from NCBI backbone (NCBIN:140576,
              NCBIP:140577)
CLASSIFICATION #superfamily retinoblastoma-associated protein
SUMMARY   #length 1139 #molecular-weight 128366 #checksum 5271

Query Match   80.6%; Score 50; DB 2; Length 1139;
Best Local Similarity   71.4%;
Matches   5; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy 50 GINLHWL 56
       |:||||
Db 81 GNDLHWL 87

Qy 50 GINLHWL 56

RESULT 15
ENTRY   A49369   #type complete

TITLE   adenovirus E1A-associated 130k protein - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE   11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change
            03-May-1996
ACCESSIONS A49369
REFERENCE   A49369
  #authors Li, Y.; Graham, C.; Lacy, S.; Duncan, A.M.V.; Whyte, P.
  #journal Genes Dev. (1993) 7:2366-2377
  #title   The adenovirus E1A-associated 130-kD protein is encoded by a
            member of the retinoblastoma gene family and physically
            interacts with cyclins A and E.
  #accession A49369
    ##status Preliminary
    ##molecule_type mRNA
    ##residues 1-1139 ##label LIA
    ##cross-references GB:X76061
CLASSIFICATION #superfamily retinoblastoma-associated protein
SUMMARY   #length 1139 #molecular-weight 128451 #checksum 5554

Query Match   80.6%; Score 50; DB 2; Length 1139;
Best Local Similarity   71.4%;
Matches   5; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy 50 GINLHWL 56
       |:||||
Db 81 GNDLHWL 87

Search completed: Tue Apr 20 14:06:29 1999
Job time : 19 secs.

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| |V| || |_  || |_  || |_| || |_| || |   || |   |
|_| |_||_____||_____||_| |_||_| |_||_____||_____| (TM)
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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 20 14:04:55 1999; MasPar time 2.51 Seconds
    74.986 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-836-455-1_1
Perfect Score: (50-56) from trans.pep (2 of 3)
Sequence: 62
   1 GINLHWL 7

Scoring table: PAM 150
   Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%
   Listing first 45 summaries

Database: swiss-prot35
   1:swissprot

Statistics: Mean 24.102;   Variance 35.768;   scale 0.674

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	53	85.5	712	1	SSK1_YEAST	OSMOLARITY TWO-COMPON	7.08e+00
2	53	85.5	1033	1	YDK9_SCHPO	HYPOTHETICAL 116.5 KD	7.08e+00
3	52	83.9	459	1	NO4M_CHICK	NADH-UBIQUINONE OXIDOR	1.05e+01
4	51	82.3	495	1	G1PK_SYNY3	GLYCEROL KINASE (EC 2.	1.55e+01
5	51	82.3	1459	1	YFIM_CAEEL	HYPOTHETICAL 166.0 KD	1.55e+01
6	50	80.6	811	1	OTU_DROME	OVARIAN TUMOR LOCUS PR	2.29e+01
7	50	80.6	1082	1	RBL2_HUMAN	RETINOBLASTOMA-LIKE PR	2.29e+01
8	49	79.0	192	1	RPC1_BP186	REPRESSOR PROTEIN CI.	3.34e+01
9	49	79.0	214	1	YNO2_PARDE	HYPOTHETICAL 22.9 KD P	3.34e+01
10	49	79.0	561	1	YD89_SCHPO	HYPOTHETICAL 63.2 KD P	3.34e+01
11	48	77.4	306	1	OPPB_ECOLI	OLIGOPEPTIDE TRANSPORT	4.87e+01
12	48	77.4	338	1	IPNS_CEPAC	ISOPENICILLIN N SYNTHE	4.87e+01
13	48	77.4	338	1	RBE_SALTI	CDP-TYVELOSE-2-EPIMERA	4.87e+01
14	48	77.4	379	1	P2X6_RAT	P2X PURINOCEPTOR 6 (AT	4.87e+01
15	48	77.4	471	1	TNAA_ECOLI	TRYPTOPHANASE (EC 4.1.	4.87e+01
16	48	77.4	760	1	TRSR_HUMAN	TRANSFERRIN RECEPTOR P	4.87e+01
17	48	77.4	810	1	UP05_ECOLI	UNKNOWN PROTEIN FROM 2	4.87e+01
18	48	77.4	1056	1	RIC1_YEAST	RIC1 PROTEIN.	4.87e+01
19	47	75.8	141	1	Y427_MYCPN	HYPOTHETICAL PROTEIN M	7.04e+01
20	47	75.8	358	1	Y4PP_RHISN	HYPOTHETICAL PROTEIN H	7.04e+01
21	47	75.8	410	1	YJTO_ECOLI	PROBABLE ABC TRANSPORT	7.04e+01
22	47	75.8	901	1	SOK1_YEAST	SOK1 PROTEIN.	7.04e+01
23	46	74.2	275	1	NRTB_SYNY3	NITRATE TRANSPORT PERM	1.01e+02
24	46	74.2	306	1	OPPB_SALTY	OLIGOPEPTIDE TRANSPORT	1.01e+02
25	46	74.2	356	1	OXDA_TRIVR	D-AMINO ACID OXIDASE (	1.01e+02
26	46	74.2	458	1	NO4M_STRCA	NADH-UBIQUINONE OXIDOR	1.01e+02
27	46	74.2	495	1	POLG_DEN23	GENOME POLYPROTEIN (MA	1.01e+02
28	46	74.2	529	1	YCR2_ERWHE	HYPOTHETICAL PROTEIN I	1.01e+02
29	46	74.2	560	1	HEMA_IATKR	HEMAGGLUTININ PRECURSO	1.01e+02
30	46	74.2	563	1	HEMA_IAFPR	HEMAGGLUTININ PRECURSO	1.01e+02
31	46	74.2	563	1	HEMA_IACKV	HEMAGGLUTININ PRECURSO	1.01e+02
32	46	74.2	563	1	HEMA_IAFPW	HEMAGGLUTININ PRECURSO	1.01e+02
33	46	74.2	563	1	HEMA_IASTA	HEMAGGLUTININ PRECURSO	1.01e+02
34	46	74.2	570	1	HEMA_IAHC6	HEMAGGLUTININ PRECURSO	1.01e+02
35	46	74.2	570	1	HEMA_IAHC5	HEMAGGLUTININ PRECURSO	1.01e+02
36	46	74.2	642	1	ARE2_YEAST	STEROL O-ACYLTRANSFERA	1.01e+02
37	46	74.2	760	1	DPP4_MOUSE	DIPEPTIDYL PEPTIDASE I	1.01e+02
38	46	74.2	766	1	DPP4_HUMAN	DIPEPTIDYL PEPTIDASE I	1.01e+02
39	46	74.2	767	1	DPP4_RAT	DIPEPTIDYL PEPTIDASE I	1.01e+02
40	46	74.2	918	1	QA1S_NEUCR	QUINATE REPRESSOR.	1.01e+02
41	46	72.6	217	1	YQIE_HAEIN	HYPOTHETICAL PROTEIN H	1.45e+02
42	46	72.6	237	1	YGGS_HAEIN	HYPOTHETICAL PROTEIN H	1.45e+02
43	45	72.6	470	1	FUCK_HAEIN	L-FUCULOKINASE (EC 2.7	1.45e+02
44	45	72.6	494	1	AMY2_SALTY	CYTOPLASMIC ALPHA-AMYL	1.45e+02
45	45	72.6	566	1	YQK4_CAEEL	HYPOTHETICAL 64.3 KD P	1.45e+02
```

ALIGNMENTS

```
RESULT 1
SSK1_YEAST          STANDARD;        PRT;    712 AA.
ID   Q07084; Q07909;
AC   Q07084;
DT   01-NOV-1997 (REL. 35, CREATED)
DT   01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   OSMOLARITY TWO-COMPONENT SYSTEM PROTEIN SSK1.
GN   SSK1 OR YLR006C.
OS   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
[1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS.
RN   MEDLINE; 94239498.
RX   MAEDA T., WURGLER-MURPHY S.M., SAITO H.;
RL   NATURE 369:242-245(1994).
[2]
RN   SEQUENCE FROM N.A.
RP   VANDENBOL M., PORTETELLE D., HILGER F.;
RA   SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
RL   -!- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
CC       SLN1/SSK1 ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE
CC       EXTRACELLULAR ENVIRONMENT. THIS SYSTEM CONTROLS THE SSK2/SSK22->
CC       PBS2->HOG1 PATHWAY. THE UNPHOSPHORYLATED FORM OF SSK1 ACTIVATES
CC       SSK2 AND SSK22, TWO MAPKKKS THAT FURTHER STIMULATE THE PBS2-HOG1
CC       MAPK CASCADE. IN LOW-OSMOLARITY MEDIA, IS INHIBITED THROUGH THE
CC       PHOSPHORYLATION BY SLN1.
CC   -!- SUBUNIT: SEEMS TO INTERACT WITH SSK2 AND SSK22.
CC   -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC   -!- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
RL   EMBL; L26523; G496306; -.
DR   EMBL; Z73178; E245767; -.
DR   SGD; L002084; SSK1.
KW   SENSORY TRANSDUCTION; PHOSPHORYLATION.
FT   DOMAIN        501    646       RECEIVER DOMAIN (POTENTIAL).
FT   MOD_RES       554    554       PHOSPHORYLATION.
FT   MUTAGEN       554    554       D->N: ACTIVATES.
FT   CONFLICT      181    181       P -> S (IN REF. 1).
SQ   SEQUENCE 712 AA;  78529 MW;  24A05B5F CRC32;
```

```
Query Match           85.5%;   Score 53;  DB 1;  Length 712;
Best Local Similarity 83.3%;   Pred. No. 7.08e+00;
Matches    5;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Db    634 VNLHWL 639
          :||||
Qy     51 INLHWL 56
```

RESULT 2

```
ID   YDK9_SCHPO     STANDARD;      PRT;   1033 AA.
AC   P87115;
DT   15-JUL-1998 (REL. 36, CREATED)
DT   15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT   15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.
GN   SPAC20G8.09C.
OS   SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   BADCOCK K., CHURCHER C.M., WOOD V., BARRELL B.G., RAJANDREAM M.A.;
RL   SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SIMILARITY: TO YEAST YNL132W AND AN A.AMBISEXUALIS HYPOTHETICAL
CC       PROTEIN (AC P54008).
DR   EMBL; Z95334; E315494; -.
KW   HYPOTHETICAL PROTEIN; ATP-BINDING.
FT   NP_BIND     282    289    ATP (POTENTIAL).
SQ   SEQUENCE   1033 AA;  116463 MW;  ACDAC931 CRC32;

Query Match             85.5%;
Best Local Similarity   83.3%;  Score 53;  DB 1;  Length 1033;
Matches   5;  Conservative   1;  Pred. No. 7.08e+00;  Mismatches  0;  Indels  0;  Gaps  0;

Db   38 VNLHWL 43
          :|||||
Qy   51 INLHWL 56
```

RESULT 3

```
ID   NU4M_CHICK     STANDARD;      PRT;   459 AA.
AC   P18939;
DT   01-NOV-1990 (REL. 16, CREATED)
DT   01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT   15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE   NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3).
GN   MTND4 OR ND4 OR NADH4.
OS   GALLUS GALLUS (CHICKEN).
OG   MITOCHONDRION.
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC   GALLIFORMES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90230301.
RA   DESJARDINS P., MORAIS R.;
RL   J. MOL. BIOL. 212:599-634(1990).
CC   -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR   EMBL; X52392; G12970; -.
DR   PIR; S10196; S10196.
KW   OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.
SQ   SEQUENCE   459 AA;  51145 MW;  8819B353 CRC32;

Query Match             83.9%;
Best Local Similarity   71.4%;  Score 52;  DB 1;  Length 459;
Matches   5;  Conservative   2;  Pred. No. 1.05e+01;  Mismatches  0;  Indels  0;  Gaps  0;

Db   36 SISLHWL 42
          :|:|||
Qy   50 GINLHWL 56
```

RESULT 4

```
ID   GLPK_SYNY3     STANDARD;      PRT;   495 AA.
AC   P74260;
DT   01-NOV-1997 (REL. 35, CREATED)
DT   01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   GLYCEROL KINASE (EC 2.7.1.30) (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE)
GN   GLPK OR SLR1672.
OS   SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC   PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
OC   CYANOBACTERIA (BLUE-GREEN ALGAE); CHROOCOCCALES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97061201.
RA   KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
RA   MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA   HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K.,
RA   OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A.,
RA   YAMADA M., YASUDA M., TABATA S.;
RL   DNA RES. 3:109-136(1996).
CC   -!- CATALYTIC ACTIVITY: ATP + GLYCEROL = ADP + GLYCEROL 3-PHOSPHATE.
CC   -!- PATHWAY: RATE-LIMITING STEP IN GLYCEROL UTILIZATION.
CC   -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE FGGY KINASE / GLUCONOKINASE /
CC       GLYCEROKINASE / XYLULOKINASE FAMILY.
DR   EMBL; D90913; G1653440; -.
DR   PROSITE; PS00933; FGGY_KINASES_1; FALSE_NEG.
DR   PROSITE; PS00445; FGGY_KINASES_2; 1.
KW   GLYCEROL METABOLISM; TRANSFERASE; KINASE.
SQ   SEQUENCE   495 AA;  54351 MW;  C7247592 CRC32;

Query Match             82.3%;
Best Local Similarity   71.4%;  Score 51;  DB 1;  Length 495;
Matches   5;  Conservative   1;  Pred. No. 1.55e+01;  Mismatches  1;  Indels  0;  Gaps  0;

Db  141 GTKLHWL 147
          |:||||
Qy   50 GINLHWL 56
```

RESULT 5

```
ID   YF1M_CAEEL     STANDARD;      PRT;   1459 AA.
AC   Q21874;
DT   15-JUL-1998 (REL. 36, CREATED)
DT   15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT   15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 166.0 KD PROTEIN R09E10.5 IN CHROMOSOME IV.
GN   R09E10.5.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRISTOL N2;
RA   MATTHEWS L.;
RL   SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SIMILARITY: STRONG, TO C.ELEGANS F54D1.6.
DR   EMBL; Z70287; E233847; -.
DR   WORMPEP; R09E10.5; CE06287.
KW   HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
SQ   SEQUENCE   1459 AA;  165994 MW;  46E17445 CRC32;

Query Match             82.3%;
Best Local Similarity   71.4%;  Score 51;  DB 1;  Length 1459;
Matches   5;  Conservative   1;  Pred. No. 1.55e+01;  Mismatches  1;  Indels  0;  Gaps  0;

Db  640 ISLHWL 645
          |:||||
Qy   51 INLHWL 56
```

RESULT 6

```
ID   OTU_DROME      STANDARD;      PRT;   811 AA.
AC   P10383;
DT   01-MAR-1989 (REL. 10, CREATED)
DT   01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
DT   01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE   OVARIAN TUMOR LOCUS PROTEIN.
GN   OTU.
OS   DROSOPHILA MELANOGASTER (FRUIT FLY).
OC   EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RC   STRAIN=CANTON-S;
RX   MEDLINE; 89263747.
RA   CHAMPE M.A., LAIRD C.D.;
RL   NUCLEIC ACIDS RES. 17:3304-3304(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90065528.
RA   STEINHAUER W.R., WALSH R.C., KALFAYAN L.J.;
RL   MOL. CELL. BIOL. 9:5726-5732(1989).
CC   -!- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR FEMALE FERTILITY.
CC   -!- SIMILARITY: LOW, WITH THE DROSOPHILA BAG-OF-MARBLES PROTEIN.
DR   EMBL; X13693; G8316; -.
DR   EMBL; M30825; G158029; -.
DR   PIR; S04085; S04085.
DR   PIR; A33829; A33829.
DR   FLYBASE; FBgn0003023; otu.
FT   CONFLICT     300    300       Q -> K (IN REF. 2).
FT   CONFLICT     789    789       T -> P (IN REF. 2).
SQ   SEQUENCE   811 AA;  92616 MW;  B8C8AC5D CRC32;

Query Match             80.6%;
Best Local Similarity   66.7%;
Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         50 GINLHW 55
              |:|||
Db        593 GVDLHW 598

Score 50;  DB 1;  Length 811;
```

```
RESULT 7
ID   RBL2_HUMAN     STANDARD;      PRT;  1082 AA.
AC   Q08999;
DT   01-NOV-1995 (REL. 32, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE   RETINOBLASTOMA-LIKE PROTEIN 2 (130 KD RETINOBLASTOMA-ASSOCIATED
DE   PROTEIN) (PRB2) (P130).
GN   RBL2 OR RB2.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93368960.
RA   MAYOL X., GRANA X., BALDI A., SANG N., HU Q., GIORDANO A.;
RL   ONCOGENE 8:2561-2566(1993).
CC   -!- FUNCTION: MAY HAVE A FUNCTION IN CELL CYCLE REGULATION. BINDS TO
CC       AND MAY BE INVOLVED IN THE TRANSFORMING CAPACITY OF THE ADENOVIRUS
CC       E1A PROTEIN. MAY ACT AS A TUMOR SUPPRESSOR. POTENT INHIBITOR OF
CC       E2F-MEDIATED TRANS-ACTIVATION, ASSOCIATES PREFERENTIALLY WITH
CC       E2F5.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SIMILARITY: BELONGS TO THE RETINOBLASTOMA PROTEIN (RB) FAMILY.
DR   EMBL; X74594; G397148; -.
DR   MIM; 180203; -.
KW   TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN; CELL CYCLE;
KW   PHOSPHORYLATION; ANTI-ONCOGENE.
FT   DOMAIN       360    967       POCKET (BINDS E1A).
FT   DOMAIN       360    559       DOMAIN A.
FT   DOMAIN       560    770       SPACER.
FT   DOMAIN       771    967       DOMAIN B.
SQ   SEQUENCE   1082 AA;  122476 MW;  4F714AE5 CRC32;

Query Match             80.6%;
Best Local Similarity   71.4%;
Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         50 GINLHWL 56
              |:|||||
Db         24 GNDLHWL 30

Score 50;  DB 1;  Length 1082;
```

```
RESULT 8
ID   RPC1_BP186     STANDARD;      PRT;   192 AA.
AC   P08707;
DT   01-JAN-1988 (REL. 06, CREATED)
DT   01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   REPRESSOR PROTEIN CI.
GN   CI.
OS   BACTERIOPHAGE 186.
OC   VIRIDAE; DS-DNA NONENVELOPED VIRUSES; MYOVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 87112711.
RA   KALIONIS B., DODD I.B., EGAN J.B.;
RL   J. MOL. BIOL. 191:199-209(1986).
CC   -!- FUNCTION: REPRESSOR OF LYSOGENY.
CC   -!- SIMILARITY: TO PHAGE HP1 CI AND TO ORFI OF E.COLI RETRON EC67.
DR   EMBL; X04449; G15554; -.
DR   PIR; S09533; S09533.
KW   TRANSCRIPTION REGULATION; REPRESSOR; DNA-BINDING.
SQ   SEQUENCE   192 AA;  21256 MW;  7D8E003E CRC32;

Query Match             79.0%;
Best Local Similarity   71.4%;
Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         50 GINLHWL 56
              |||:|||
Db         62 GANLQWL 68

Score 49;  DB 1;  Length 192;
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```
RESULT 9
ID   YN02_PARDE     STANDARD;      PRT;   214 AA.
AC   P29908;
DT   01-APR-1993 (REL. 25, CREATED)
DT   01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT   01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 22.9 KD PROTEIN IN NQO2 3'REGION (URF2).
OS   PARACOCCUS DENITRIFICANS.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC   UNCERTAIN.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 13548;
RX   MEDLINE; 91563357.
RA   XU X., MATSUNO-YAGI A., YAGI T.;
RL   BIOCHEMISTRY 30:8678-8684(1991).
CC   -!- FUNCTION: URF2 PRODUCT MAY BE INVOLVED IN THE TRANSFER OF IRON-
CC       SULFUR CLUSTERS TO THE NADH DEHYDROGENASE COMPLEX. IT MAY ALSO
CC       BE REQUIRED FOR THE ASSEMBLY OF THE NADH DEHYDROGENASE COMPLEX.
CC   -!- SIMILARITY: SIGNIFICANT TO ORF3 OF P.DENITRIFICANS (LOCATED
CC       BETWEEN THE COX11 & COX111 GENES).
DR   EMBL; M74171; G150604; -.
DR   PIR; B42096; B42096.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   214 AA;  22906 MW;  DA6A9F8A CRC32;

Query Match             79.0%;
Best Local Similarity   75.0%;
Matches    6;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         50 GI-NLHWL 56
              || :||||
Db         27 GIGDLHWL 34

Score 49;  DB 1;  Length 214;
```

```
RESULT 10
ID   YD89_SCHPO     STANDARD;      PRT;   561 AA.
AC   Q10414;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
```

DE   HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN-CHROMOSOME I.
GN   SPAC1F3.09.
OS   SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RA   CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
RL   SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- SIMILARITY: TO YEAST YGR093W.
DR   EMBL; Z70690; E234475; -.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE 561 AA; 63216 MW; EB2F8868 CRC32;

Query Match   Best Local Similarity 79.0%;   Score 49; DB 1; Length 561;
                                    66.7%;   Pred. No. 3.34e+01;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 447 GVHLEW 452
         |::|||
Qy   50 GINLHW 55

RESULT 11
ID   OPPB_ECOLI   STANDARD;   PRT;   306 AA.
AC   P31132; P76026; P77550;
DT   01-JUL-1993 (REL. 26, CREATED)
DT   01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPB.
OS   ESCHERICHIA COLI.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   ENTEROBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RA   BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
RL   SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RA   AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,
RA   IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
RA   KASHIMOTO K., KIM S., KIMURA S., KITAGAWA M., KITAKAWA M., MAKINO K.,
RA   MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y.,
RA   NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,
RA   TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.;
RL   SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [3]
RP   SEQUENCE OF 1-16 FROM N.A.
RX   MEDLINE; 90256748.
RA   KASHIWAGI K., YAMAGUCHI Y., SAKAI Y., KOBAYASHI H., IGARASHI K.;
RL   J. BIOL. CHEM. 265:8387-8391(1990).
CC   -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC   FOR OLIGOPEPTIDES; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF
CC   THE SUBSTRATE ACROSS THE MEMBRANE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
CC   -!- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC   PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPBC
CC   SUBFAMILY.
DR   EMBL; AE000223; G1887497; -.
DR   EMBL; D90763; G1742033; -.
DR   EMBL; D90852; D1017767; -.
DR   EMBL; J05433; -; NOT_ANNOTATED_CDS.
DR   PIR; B36263; B36263.
DR   ECOGENE; EG10675; OPPB.
DR   PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
KW   TRANSPORT; PEPTIDE TRANSPORT; TRANSMEMBRANE; INNER MEMBRANE.
FT   DOMAIN   1   9   CYTOPLASMIC (PROBABLE).
FT   TRANSMEM   10   30   PROBABLE.
FT   DOMAIN   31   99   EXTRACELLULAR (PROBABLE).
FT   TRANSMEM 100   121   PROBABLE.
FT   DOMAIN   122   137   CYTOPLASMIC (PROBABLE).
FT   TRANSMEM 138   158   PROBABLE.
FT   DOMAIN   159   172   EXTRACELLULAR (PROBABLE).
FT   TRANSMEM 173   190   PROBABLE.
FT   DOMAIN   191   226   CYTOPLASMIC (PROBABLE).
FT   TRANSMEM 227   250   PROBABLE.
FT   DOMAIN   251   271   EXTRACELLULAR (PROBABLE).
FT   TRANSMEM 272   293   PROBABLE.
FT   DOMAIN   294   306   CYTOPLASMIC (PROBABLE).
SQ   SEQUENCE 306 AA; 33443 MW; 3FCCC9F5 CRC32;

Query Match   Best Local Similarity 77.4%;   Score 48; DB 1; Length 306;
                                    71.4%;   Pred. No. 4.87e+01;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 155 AIILHWL 161
         :| ||||
Qy   50 GINLHWL 56

RESULT 12
ID   IPNS_CEPAC   STANDARD;   PRT;   338 AA.
AC   P05189;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   ISOPENICILLIN N SYNTHETASE (IPNS).
GN   PCBC OR IPS.
OS   CEPHALOSPORIUM ACREMONIUM (ACREMONIUM CHRYSOGENUM).
OC   EUKARYOTA; FUNGI; ASCOMYCOTINA; PLECTOMYCETES; EUROTIALES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 86040479.
RA   SAMSON S.N., BELAGAJE R., BLANKENSHIP D.T., CHAPMAN J.L., PERRY D.,
RA   SKATRUD P.L., VANFRANK R.M., ABRAHAM E.P., BALDWIN J.E., QUEENER S.W.,
RA   INGOLIA T.D.;
RL   NATURE 318:191-194(1985).
RN   [2]
RP   SEQUENCE OF 3-52.
RC   STRAIN=ATCC 60777;
RX   MEDLINE; 85285585.
RA   BALDWIN J.E., GAGNON J., TING H.H.;
RL   FEBS LETT. 188:253-256(1985).
RN   [3]
RP   SEQUENCE OF 40-78 AND 237-264, AND PHOTOAFFINITY LABELLING.
RX   MEDLINE; 90197638.
RA   BALDWIN J.E., COATES J.B., MOLONEY M.G., PRATT A.J., WILLIS A.C.;
RL   BIOCHEM. J. 266:561-567(1990).
CC   -!- CATALYTIC ACTIVITY: REMOVES, IN THE PRESENCE OF OXYGEN, 4 HYDROGEN
CC   ATOMS FROM L-(ALPHA-AMINOADIPYL)-L-CYSTEINYL-D-VALINE TO FORM THE
CC   AZETIDINONE AND THIAZOLIDINE RINGS OF ISOPENICILLIN.
CC   -!- COFACTOR: IRON AND ASCORBATE.
CC   -!- PATHWAY: CENTRAL ROLE IN THE BIOSYNTHESIS OF PENICILLIN AND
CC   CEPHALOSPORIN.
CC   -!- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
CC   OXIDOREDUCTASES.
DR   EMBL; X03148; G25006; -.
DR   PIR; A24567; A24567.
DR   PIR; A23995; A23995.
DR   PIR; S09312; S09312.
DR   PROSITE; PS00185; IPNS_1; 1.
DR   PROSITE; PS00186; IPNS_2; 1.
KW   ANTIBIOTIC BIOSYNTHESIS; OXIDOREDUCTASE; IRON; VITAMIN C.
FT   CONFLICT   22   22   D -> T (IN REF. 2).
SQ   SEQUENCE 338 AA; 38433 MW; EE264220 CRC32;

Query Match   Best Local Similarity 77.4%;   Score 48; DB 1; Length 338;
                                    57.1%;   Pred. No. 4.87e+01;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db   50 GVDLPWL 56
         |:|| ||
Qy   50 GINLHWL 56

RESULT 13
```
ID   RFBE_SALTI    STANDARD;    PRT;   338 AA.
AC   P14169;
DT   01-JAN-1990 (REL. 13, CREATED)
DT   01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT   01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE   CDP-TYVELOSE-2-EPIMERASE (EC 5.1.3.-).
GN   RFBE.
OS   SALMONELLA TYPHI.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   ENTEROBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TY2;
RX   MEDLINE; 90008813.
RA   VERMA N., REEVES P.R.;
RL   J. BACTERIOL. 171:5694-5701(1989).
RN   [2]
RA   REEVES P.R.;
RL   SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- CATALYTIC ACTIVITY: CDP-PARATOSE = CDP-TYVELOSE.
CC   -!- PATHWAY: FINAL STEP IN THE BIOSYNTHETIC PATHWAY OF CDP-TYVELOSE.
CC   -!- SIMILARITY: TO ABEQUOSE AND PARATOSE SYNTHASES AND TO UDP-
CC       GLUCOSE-4-EPIMERASE OF E.COLI.
DR   EMBL; M29682; G861175; -.
DR   PIR; B33604; B33604.
KW   LIPOPOLYSACCHARIDE BIOSYNTHESIS; ISOMERASE.
SQ   SEQUENCE  338 AA;  37958 MW;  12C22DD0 CRC32;

Query Match   77.4%;   Score 48;  DB 1;  Length 338;
Best Local Similarity 100.0%;  Pred. No. 4.87e+01;
Matches    5;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Db    41 NLHWL 45
         |||||
Qy    52 NLHWL 56
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RESULT 14
```
ID   P2X6_RAT    STANDARD;    PRT;   379 AA.
AC   P51579;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE   P2X PURINOCEPTOR 6 (ATP RECEPTOR) (P2X6) (PURINERGIC RECEPTOR).
GN   P2RX6.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CERVICAL GANGLION;
RX   MEDLINE; 96256686.
RA   COLLO G., KAWASHIMA E., PICH E., NEIDHART S., NORTH R.A.,
RA   SURPRENANT A., BUELL G.N.;
RL   J. NEUROSCI. 16:2495-2507(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX   MEDLINE; 96264662.
RA   SOTO F., GARCIA-GUZMAN M., KARSCHIN C., STUEHMER W.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 223:456-460(1996).
CC   -!- FUNCTION: RECEPTOR FOR ATP THAT ACTS AS A LIGAND GATED ION
CC       CHANNEL.
CC   -!- SUBUNIT: HOMO- OR HETEROPOLYMERS (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE P2X RECEPTOR FAMILY.
DR   EMBL; X97376; E242827; -.
DR   EMBL; X92070; E205329; -.
DR   PROSITE; PS01212; P2X_RECEPTOR; 1.
KW   IONIC CHANNEL; TRANSMEMBRANE; ION TRANSPORT; RECEPTOR; GLYCOPROTEIN.
FT   DOMAIN        1     31       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     32     52       1 (POTENTIAL).
FT   DOMAIN       53    325       EXTRACELLULAR, CYSTEINE-RICH (POTENTIAL).
FT   TRANSMEM    326    346       2 (POTENTIAL).
FT   DOMAIN      347    379       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    157    157       POTENTIAL.
FT   CARBOHYD    187    187       POTENTIAL.
FT   CARBOHYD    202    202       POTENTIAL.
SQ   SEQUENCE  379 AA;  42450 MW;  BB28C0D0 CRC32;

Query Match   77.4%;   Score 48;  DB 1;  Length 379;
Best Local Similarity 83.3%;  Pred. No. 4.87e+01;
Matches    5;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Db   257 GINIHW 262
         |||:||
Qy    50 GINLHW 55
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RESULT 15
```
ID   TNAA_ECOLI   STANDARD;   PRT;   471 AA.
AC   P00913; P78123;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT   15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE   TRYPTOPHANASE (EC 4.1.99.1) (L-TRYPTOPHAN INDOLE-LYASE) (TNASE).
GN   TNAA OR IND.
OS   ESCHERICHIA COLI.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   ENTEROBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE; 82007678.
RA   DEELEY M.C., YANOFSKY C.;
RL   J. BACTERIOL. 147:787-796(1981).
RN   [2]
RP   SEQUENCE FROM N.A., AND IMPORTANCE OF CYS-298.
RX   MEDLINE; 89323226.
RA   TOKUSHIGE M., TSUJIMOTO N., ODA T., HONDA T., YUMOTO N., ITO S.,
RA   YAMAMOTO M., KIM E.H., HIRAGI Y.;
RL   BIOCHIMIE 71:711-720(1989).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE; 93315143.
RA   BURLAND V.D., PLUNKETT G. III, DANIELS D.L., BLATTNER F.R.;
RL   GENOMICS 16:551-561(1993).
RN   [4]
RP   SEQUENCE OF TRYPTIC PEPTIDES.
RX   MEDLINE; 72134434.
RA   KAGAMIYAMA H., MATSUBARA H., SNELL E.E.;
RL   J. BIOL. CHEM. 247:1576-1586(1972).
RN   [5]
RP   SEQUENCE OF 1-21 FROM N.A.
RC   STRAIN=K12;
RX   MEDLINE; 86033634.
RA   STEWART V., YANOFSKY C.;
RL   J. BACTERIOL. 164:731-740(1985).
RN   [6]
RP   SEQUENCE OF 463-471 FROM N.A.
RX   MEDLINE; 91216998.
RA   SARSERO J.P., WOOKEY P.J., GOLLNICK P.D., YANOFSKY C., PITTARD A.J.;
RL   J. BACTERIOL. 173:3231-3234(1991).
RN   [7]
RP   SEQUENCE OF 1-12.
RC   STRAIN=K12 / EMG2;
RA   LINK A.J.;
RL   SUBMITTED (OCT-1994) TO THE SWISS-PROT DATA BANK.
RN   [8]
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RP   MUTAGENESIS OF CYS-294 AND CYS-298.
RX   MEDLINE; 89278130.
RA   PHILLIPS R.S., GOLLNICK P.D.;
RL   J. BIOL. CHEM. 264:10627-10632(1989).
-!- CATALYTIC ACTIVITY: L-TRYPTOPHAN + H(2)O = INDOLE + PYRUVATE +
      NH(3) (ALSO CATALYZES THE SYNTHESIS OF TRYPTOPHAN FROM INDOLE
      AND SERINE).
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMOTETRAMER.
-!- SIMILARITY: HIGH, TO TYROSINE PHENOL-LYASE.
EMBL; K00032; G147997; -.
EMBL; X15974; G41936; -.
EMBL; M11990; G148001; -.
EMBL; M59914; -; NOT_ANNOTATED_CDS.
EMBL; L10328; G290556; ALT_INIT.
EMBL; AE000448; G1790144; ALT_INIT.
PIR; A01136; WZEC.
HSSP; P31013; 1TPL.
EC02DBASE; G046.5; 6TH EDITION.
ECOGENE; EG11005; TNAA.
PROSITE; PS00853; BETA_ELIM_LYASE; 1.
TRYPTOPHAN BIOSYNTHESIS; LYASE; PYRIDOXAL PHOSPHATE.
KW   PYRIDOXAL PHOSPHATE.
FT   BINDING    270    270    PYRIDOXAL PHOSPHATE.
FT   MUTAGEN    294    294    C->S: IDENTICAL TO WILD-TYPE.
FT   MUTAGEN    298    298    C->S: ALTERED ACTIVITY.
FT   CONFLICT   137    140    D->TQ -> TTQG (IN REF. 1).
FT   CONFLICT   379    380    QA -> TG (IN REF. 1 AND 2).
SQ   SEQUENCE  471 AA;   52773 MW;  3724A677 CRC32;
```

Query Match   77.4%;   Score 48;   DB 1;   Length 471;
Best Local Similarity   71.4%;   Pred. No. 4.87e+01;
Matches   5;   Conservative   1;   Mismatches 1;   Indels 0;   Gaps 0;

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Db    325 GMNLDWL 331
          |:||| ||
Qy     50 GINLHWL 56
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Search completed: Tue Apr 20 14:05:02 1999
Job time : 7 secs.

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 20 14:05:20 1999; MasPar time 4.35 Seconds
                                          80.112 Million cell updates/sec

Title:
Description: >US-08-836-455-1_1
Perfect Score: 62   (50-56) from trans.pep (2 of 3)
Sequence: 1 GINLHWL 7

Tabular output not generated.

Database: sptrembl6

Statistics: Mean 23.380; Variance 35.189; scale 0.664
                 1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
                 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
                 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
                 13:sp_vertebrate 14:sp_virus

Scoring table: PAM 150
                 Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES

Result   %   Query
No. Score Match Length DB ID   Description   Pred. No.
---- ----- ----- ------ -- --------   -----------   --------
  1   58   93.5   964   2   053784   PUTATIVE MEMBRANE PROT   1.45e+00
  2   53   85.5   967   2   053735   PUTATIVE TRANSMEMBRANE   1.15e-01
  3   50   80.6   198   2   P71161   INTB, REGA, GEPA, GEPB   3.74e+01
  4   50   80.6   372   2   P95233   HYPOTHETICAL 41.3 KD P   3.74e+01
  5   50   80.6   386   11   060962   CARCINOEMBRYONIC ANTIG   3.74e+01
  6   50   80.6   435   5   021859   R09D1.3.   3.74e+01
  7   50   80.6   687   2   067845   GLUTAMATE SYNTHASE SMA   3.74e+01
  8   50   80.6   687   2   005069   TRANSPOSASE A (MUA)   3.74e+01
  9   50   80.6   707   2   050198   TONB-DEPENDENT RECEPTO   3.74e+01
 10   50   80.6   791   2   025543   IRON-REGULATED OUTER M   3.74e+01
 11   50   80.6   1135   11   064700   RETINOBLASTOMA-LIKE 2   3.74e+01
 12   50   80.6   1135   11   055081   P130.   3.74e+01
 13   50   80.6   1135   11   016084   P130.   3.74e+01
 14   50   80.6   1139   4   015073   130K PROTEIN.   3.74e+01
 15   49   79.0   1139   4   051122   HEPTOSYLTRANSFERASE I.   5.49e+01
 16   49   79.0   322   2   050937   LIPOOLIGOSACCHARIDE HE   5.49e+01
 17   49   79.0   326   2   051128   1,5 HEPTOSYLTRANSFERAS   5.49e+01
 18   49   79.0   332   2   050177   SUCCINYLGLUTAMATE DESU   5.49e+01
 19   49   79.0   391   2   P73167   HYPOTHETICAL 42.6 KD P   5.49e+01
 20   49   79.0   521   5   021360   K08F8.1.   5.49e+01
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Left column

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DT   01-JUN-1998 (TREMBLREL, 06, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL, 06, LAST ANNOTATION UPDATE)
DE   PUTATIVE TRANSMEMBRANE PROTEIN.
GN   MTV037.14C.
OS   MYCOBACTERIUM TUBERCULOSIS.
OC   PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   BROWN D., CHURCHER C.M.;
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H37RV;
RL   SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
RA   COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H37RV;
RL   SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RA   COLE S.T., EIGLMEIER K., PASCOPELLA L.,
RA   BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
RA   PHILIPP W.J., POULET S.,
RX   MEDLINE; 96181548.
DR   EMBL; AL021932; E1252519; -.
KW   TRANSMEMBRANE.
SQ   SEQUENCE   967 AA;  105233 MW;  3957DF42 CRC32;

Qy      50  GINLHWL  56
            :|:||||
Db     823  AIHLHWL  829

Query Match             85.5%;   Score 53;  DB 2;  Length 967;
Best Local Similarity   71.4%;
Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
                                   Pred. No. 1.15e+01;
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RESULT 3
ID   P71161
AC   P71161;
DT   01-FEB-1997 (TREMBLREL, 02, CREATED)
DT   01-FEB-1997 (TREMBLREL, 02, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL, 07, LAST ANNOTATION UPDATE)
DE   INTB, REGA, GEPA, GEPB, AND GEPC GENES.
GN   GEPB.
OS   BACTEROIDES NODOSUS (DICHELOBACTER NODOSUS).
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; ANAEROBIC RODS;
OC   BACTEROIDACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A198;
RA   BLOOMFIELD G.A., WHITTLE G., MCDONAGH M.B., KATZ M.E., CHEETHAM B.F.;
RL   MICROBIOLOGY 143:553-562(1997).
DR   EMBL; X98546; E258655; -.
SQ   SEQUENCE   198 AA;   21550 MW;  FA6F6C9D CRC32;

Qy      51  INLHWL  56
            ||||||
Db     157  ITLHWL  162

Query Match             80.6%;   Score 50;  DB 2;  Length 198;
Best Local Similarity   83.3%;
Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
                                   Pred. No. 3.74e+01;
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RESULT 4
ID   P95233
AC   P95233;
DT   01-MAY-1997 (TREMBLREL, 03, CREATED)
DT   01-MAY-1997 (TREMBLREL, 03, LAST SEQUENCE UPDATE)
DT   01-MAY-1997 (TREMBLREL, 03, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 41.3 KD PROTEIN.
GN   MTCY98.06C.
                                        PRELIMINARY;  PRT;  372 AA.
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Right column

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OS   MYCOBACTERIUM TUBERCULOSIS.
OC   PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   BROWN D., CHURCHER C.M.;
RN   [2]
RP   SEQUENCE FROM N.A.
RL   SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RA   COLE S.T., BARRELL B.G., RAJANDREAM M.A.;
RN   [3]
RP   SEQUENCE FROM N.A.
RL   SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RA   COLE S.T., BARRELL B.G., RAJANDREAM M.A.;
RA   BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
RA   PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
RX   MEDLINE; 96181548.
RL   PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
DR   EMBL; Z83860; E290744; -.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE   372 AA;   41272 MW;  A4F94BDE CRC32;

Qy      50  GINLHWL  56
            ||:||:|
Db     154  GIQLHWF  160

Query Match             80.6%;   Score 50;  DB 2;  Length 372;
Best Local Similarity   71.4%;
Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
                                   Pred. No. 3.74e+01;
```

```
RESULT 5
ID   Q60962
AC   Q60962;
DT   01-NOV-1996 (TREMBLREL, 01, CREATED)
DT   01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL, 06, LAST ANNOTATION UPDATE)
DE   CARCINOEMBRYONIC ANTIGEN 11 (BRAIN CARCINOEMBRYONIC ANTIGEN).
GN   CEA11 OR BCEA.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 96109212.
RA   CHEN D.S., ASANAKA M., YOKOMORI K., WANG F., HWANG S.B., LI H.P.,
RA   LAI M.M.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 92:12095-12099(1995).
DR   EMBL; U34272; G1098896; -.
DR   MGD; MGI:104983; CEA11.
DR   PFAM; PF00047; 1g.
SQ   SEQUENCE   386 AA;   43362 MW;  E1EA398E CRC32;

Qy      50  GINLHWL  56
            |:||:|||
Db     323  GVSIHWL  329

Query Match             80.6%;   Score 50;  DB 11;  Length 386;
Best Local Similarity   57.1%;
Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;
                                   Pred. No. 3.74e+01;
```

```
RESULT 6
ID   Q21859
AC   Q21859;
DT   01-NOV-1996 (TREMBLREL, 01, CREATED)
DT   01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL, 07, LAST ANNOTATION UPDATE)
DE   R09D1.3.
OS   CAENORHABDITIS ELEGANS.
OC   EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN   [1]
RP   SEQUENCE FROM N.A.
                                        PRELIMINARY;  PRT;  435 AA.

Qy      50  GINLHWL  56
```

```
RA   MATTHEWS P.;
RL   SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
RA   BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M.,
RA   DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P.,
RA   HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,
RA   KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
RA   MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,
RA   RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A.,
RA   SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K.,
RA   VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
RA   WILKINSON-SPROAT J., WOHLDMAN P.;
RL   NATURE 368:32-38(1994).
DR   EMBL; Z70035; E28187; -.
DR   PFAM; PF00704; glycosyl_hydro8.
SQ   SEQUENCE 435 AA; 50487 MW; C05D5854 CRC32;

Query Match     Best Local Similarity   66.7%;
Matches   4;   Conservative   2;   Mismatches   0;   Indels   0;   Gaps   0;
                                Score 50;   DB 5;   Length 435;
                                Pred. No. 3.74e+01;

Db    182  GVDLHW  187
            |.:|||
Qy     50  GINLHW   55


RESULT 7
ID   067845
AC   067845;
DT   01-AUG-1998 (TREMBLREL. 07, CREATED)
DT   01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   GLUTAMATE SYNTHASE SMALL SUBUNIT GLTD.
GN   GLTD.
OS   AQUIFEX AEOLICUS.
OC   EUBACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VF5;
RA   DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RA   GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
RA   FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
RL   NATURE 392:353-358(1998).
SQ   SEQUENCE 476 AA; 52947 MW; 97B08285 CRC32;

                    PRELIMINARY;   PRT;   476 AA.

Query Match     Best Local Similarity   57.1%;
Matches   4;   Conservative   3;   Mismatches   0;   Indels   0;   Gaps   0;
                                Score 50;   DB 2;   Length 476;
                                Pred. No. 3.74e+01;

Db    342  GVKIHWL  348
            |.::|||
Qy     50  GINLHWL   56


RESULT 8
ID   005069
AC   005069;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)
DE   TRANSPOSASE A (MUA).
GN   HI1478.
OS   HAEMOPHILUS INFLUENZAE.
```

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OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC   PASTEURELLACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95350630.
RA   FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA   KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M.,
RA   MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
RA   SCOTT J.D., SHIRLEY R., LIU L.I., GLODEK A., KELLEY J.M., WEIDMAN J.F.,
RA   PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R.,
RA   HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D.,
RA   FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L.,
RA   MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O., VENTER J.C.;
RL   SCIENCE 269:496-512(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   L TATUSOV R., MUSHEGIAN A.R., BORK P., BROWN N.P., HAYES W.S.,
RA   BORODOVSKY M., RUDD K.E., KOONIN E.V.;
RL   CURR. BIOL. 6:279-291(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA   KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M.,
RA   MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
RA   SCOTT J.D., SHIRLEY R., LIU L.I., GLODEK A., KELLEY J.M., WEIDMAN J.F.,
RA   PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R.,
RA   HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D.,
RA   FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L.,
RA   MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O., VENTER J.C.;
RL   SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   WHITE O., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
RL   SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U32825; G1574318; -.
SQ   SEQUENCE 687 AA; 78719 MW; A4C0045E CRC32;

Query Match     Best Local Similarity   83.3%;
Matches   5;   Conservative   1;   Mismatches   0;   Indels   0;   Gaps   0;
                                Score 50;   DB 2;   Length 687;
                                Pred. No. 3.74e+01;

Db    379  GIELHW  384
            ||:|||
Qy     50  GINLHW   55


RESULT 9
ID   050198
AC   050198;
DT   01-JUN-1998 (TREMBLREL. 06, CREATED)
DT   01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   TONB-DEPENDENT RECEPTOR HOMOLOG (FRAGMENT).
OS   HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
OC   AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RU1;
RA   MANOS J., KOLESNIKOW T., HAZELL S.L.;
RL   SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; AF015886; G2665532; -.
FT   NON_TER   707   707
SQ   SEQUENCE 707 AA; 79095 MW; B82B1B54 CRC32;

                    PRELIMINARY;   PRT;   707 AA.

Query Match     Best Local Similarity   85.7%;
Matches   6;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;
                                Score 50;   DB 2;   Length 707;
                                Pred. No. 3.74e+01;

Db    665  GINLAWL  671
            ||:||||
Qy     50  GINLHWL   56
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                    PRELIMINARY;   PRT;   687 AA.
```

RESULT 10

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ID   Q25543     PRELIMINARY;     PRT;     791 AA.
AC   Q25543;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   IRON-REGULATED OUTER MEMBRANE PROTEIN (FRPB).
GN   HP0876.
OS   HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
OC   AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=26695;
RX   MEDLINE; 97394467.
RA   TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
RA   FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
RA   NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
RA   LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,
RA   MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
RA   BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
RA   COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E.,
RA   HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
RA   VENTER J.C.;
RL   NATURE 388:539-547(1997).
DR   EMBL; AE000597; G2314011; -.
DR   TIGR; HP0876; -.
KW   HYPOTHETICAL PROTEIN.
SQ   SEQUENCE  791 AA;  88525 MW;  CBE14740 CRC32;

Query Match    80.6%;    Score 50;   DB 2;  Length 791;
Best Local Similarity  85.7%;  Pred. No. 3.74e+01;
Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Db          665 GINLAWL 671
                |||| ||
Qy           50 GINLHWL 56
```

RESULT 11

```
ID   Q64700     PRELIMINARY;     PRT;     1135 AA.
AC   Q64700;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   RETINOBLASTOMA-LIKE 2 (RETINOBLASTOMA-LIKE PROTEIN 2 .
DE   RBL2 OR P130) (RETINOBLASTOMA-RELATED PROTEIN P130)
DE   (RETINOBLASTOMA-RELATED PROTEIN PRB2/P130) (RB-RELATED P130).
GN   RBL2.
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   CHEN G., GUY C.T., CHEN H.W., HU N., LEE E.Y.H.P., LEE W.H.;
RX   MEDLINE; 96199216.
RL   J. BIOL. CHEM. 271:9567-9572(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96192345.
RA   PERTILE P., BALDI A., DE LUCA A., VIRGILIO L., PISANO M.M.,
RA   GIORDANO A.;
RL   CELL GROWTH DIFFER. 6:1659-1664(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   LECOUTER J.E., WHITE P.F.M., RUDNICKI M.A.;
RX   MEDLINE; 96203998.
RL   ONCOGENE 12:1433-1440(1996).
DR   EMBL; U36799; G1045520; -.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR.
CC   -!- SIMILARITY: BELONGS TO THE RETINOBLASTOMA PROTEIN (RB) FAMILY.
DR   EMBL; U50850; G1255232; -.
DR   EMBL; U47333; G1185008; -.
DR   MGD; MGI:105085; RBL2.
KW   NUCLEAR PROTEIN.
FT   CONFLICT      211    253    MISSING (IN REF. 3).
FT   CONFLICT      341    341    A -> P (IN REF. 2).
FT   CONFLICT      342    342    A -> P (IN REF. 3).
FT   CONFLICT      381    381    T -> P (IN REF. 2 AND 3).
FT   CONFLICT      428    428    S -> T (IN REF. 2 AND 3).
FT   CONFLICT      431    431    S -> T (IN REF. 2 AND 3).
FT   CONFLICT      443    443    Q -> R (IN REF. 2 AND 3).
FT   CONFLICT      484    493    MISSING (IN REF. 2).
FT   CONFLICT      768    768    R -> A (IN REF. 2 AND 3).
FT   CONFLICT      826    826    P -> A (IN REF. 3).
FT   CONFLICT      947    948    PT -> RA (IN REF. 3).
FT   CONFLICT     1023   1023    S -> A (IN REF. 2 AND 3).
FT   CONFLICT     1044   1044    I -> V (IN REF. 2 AND 3).
SQ   SEQUENCE  1135 AA;  127516 MW;  B77FFAF3 CRC32;

Query Match    80.6%;    Score 50;   DB 11;  Length 1135;
Best Local Similarity  71.4%;  Pred. No. 3.74e+01;
Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Db           78 GNDLHWL 84
                | :||||
Qy           50 GINLHWL 56
```

RESULT 12

```
ID   Q55081     PRELIMINARY;     PRT;     1135 AA.
AC   Q55081;
DT   01-JUN-1998 (TREMBLREL. 06, CREATED)
DT   01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT   01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE   P130.
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=SPLEEN;
RA   SAWADA Y., NOMURA H., ENDO Y., UMEKI K., FUJITA T., OHTAKI S.,
RA   FUJINAGA K.;
RL   BIOCHIM. BIOPHYS. ACTA 1361:20-27(1997).
DR   EMBL; D55627; D1025106; -.
SQ   SEQUENCE  1135 AA;  127816 MW;  369B2AAB CRC32;

Query Match    80.6%;    Score 50;   DB 11;  Length 1135;
Best Local Similarity  71.4%;  Pred. No. 3.74e+01;
Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Db           78 GNDLHWL 84
                | :||||
Qy           50 GINLHWL 56
```

RESULT 13

```
ID   Q16084     PRELIMINARY;     PRT;     1139 AA.
AC   Q16084;
DT   01-NOV-1996 (TREMBLREL. 01, CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   P130.
DE   RBR-2.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94074896.
RA   HANNON G.J., DEMETRICK D., BEACH D.;
RL   GENES DEV. 7:2378-2391(1993).
DR   EMBL; S67171; G453132; -.
```

```
SQ  SEQUENCE  1139 AA;  128365 MW;  2F0C942B CRC32;

Query Match            80.6%;  Score 50;  DB 4;  Length 1139;
Best Local Similarity  71.4%;  Pred. No. 3.74e+01;
Matches  5;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;

Db     81 GNDLHWL 87
           | :|||||
Qy     50 GINLHWL 56


RESULT  14
ID   Q15073             PRELIMINARY;       PRT;  1139 AA.
AC   Q15073;
DT   01-NOV-1996 (TREMBLREL. 01; CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE   130K PROTEIN.
GN   P130.
OC   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA /SPLEEN;
RX   MEDLINE; 94074895.
RA   LI Y., GRAHAM C., LACY S., DUNCAN A.M.V., WHYTE P.;
RL   GENES DEV. 7:2366-2377(1993).
DR   EMBL; X76061; G416031; -.
SQ   SEQUENCE 1139 AA;  128381 MW;  659C515E CRC32;

Query Match            80.6%;  Score 50;  DB 4;  Length 1139;
Best Local Similarity  71.4%;  Pred. No. 3.74e+01;
Matches  5;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;

Db     81 GNDLHWL 87
           | :|||||
Qy     50 GINLHWL 56


RESULT  15
ID   Q51122             PRELIMINARY;       PRT;  322 AA.
AC   Q51122;
DT   01-NOV-1996 (TREMBLREL. 01; CREATED)
DT   01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT   01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE   HEPTOSYLTRANSFERASE I.
RFAC.
OC   NEISSERIA MENINGITIDIS.
OC   PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
OC   NEISSERIACEAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   ZHOU D., LEE F.F., APICELLA M.A.;
RL   SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U35454; G1016752; -.
KW   TRANSFERASE.
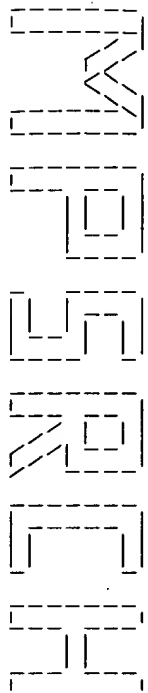SQ   SEQUENCE 322 AA;  36188 MW;  8278FA9F CRC32;

Query Match            79.0%;  Score 49;  DB 2;  Length 322;
Best Local Similarity  66.7%;  Pred. No. 5.49e+01;
Matches  4;  Conservative  2;  Mismatches  0;  Indels  0;  Gaps  0;

Db     31 VELHWL 36
           ::||||
Qy     51 INLHWL 56


Search completed: Tue Apr 20 14:05:51 1999
Job time : 31 secs.
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          M P S R C H                      (TM)

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 20 14:08:59 1999; MasPar time 2.57 Seconds
                                              56.748 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-836-455-1_1
                (89-97) from trans.pep (3 of 3)
Perfect Score: 54
Sequence: 1 SDYSLTISS 9

Scoring table: PAM 150
                Gap 11

Searched: 13192 seqs, 16180660 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: a-geneseq32
                1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
                8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
                14:part14 15:part15 16:part16 17:part17 18:part18
                19:part19 20:part20 21:part21 22:part22 23:part23
                24:part24 25:part25 26:part26 27:part27 28:part28
                29:part29

Statistics: Mean 15.830; Variance 48.580; scale 0.326

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES

                                %
Result   Query
No.   Score   Match Length DB ID   Description   Pred. No.
----- -----   ------------ -- --   -----------   --------
 1   54   100.0   95 25 W18269   PrP 81 light chain va   1.90e+01
 2   54   100.0 107 29 W44122   Light chain variable   1.90e+01
 3   54   100.0 107 25 W27121   Murine antibody light   1.90e+01
 4   54   100.0 108 4 R21310   Light chain of Mif cl   1.90e+01
 5   54   100.0 108 25 R21286   Murine VL kappa group   1.90e+01
 6   54   100.0 109 25 W18271   Murine Vl light chain va   1.90e+01
 7   54   100.0 109 18 R52030   Prp 37 light chain va   1.90e+01
 8   54   100.0 129 24 W22537   Light chain variable   1.90e+01
 9   54   100.0 145 25 W27119   Murine anti-human cla   1.90e+01
10   54   100.0 146 4 P30251   Murine monoclonal ant   1.90e+01
11   54   100.0 243 18 W02280   Sequence of the leade   1.90e+01
12   54   100.0 246 8 R39569   Sequence of G-FIT.   1.90e+01
13   54   100.0 534 8 R39571   52O9 anti-c-erbB-2 t   1.90e+01
14   52   96.3 107 29 W44123   Sequence of 52O9 SFV   1.90e+01
15   52   96.3 127 6 R32125   Light chain variable   3.15e+01
16   52   96.3 144 3 R15322   Anti-IL2R alpha antib   3.15e+01
17   52   96.3 144 3 R15321   IL-2 chimeric antibod   3.15e+01
18   51   94.4 107 14 R79247   Light chain variable   4.05e+01
19   51   94.4 107 14 R78972   Light chain variable   4.05e+01
20   51   94.4 107 14 R79250   Light chain variable   4.05e+01
21   50   92.6 106 28 W31647   Monoclonal antibody C   5.19e+01
22   50   92.6 107 29 W23956   Mus musculus A717 ant   5.19e+01
23   50   92.6 107 25 W24515   Anti-Factor-IX humani   5.19e+01
24   50   92.6 109 26 W24530   Anti-Factor-IX humani   5.19e+01
25   50   92.6 109 26 W29997   Humanised variant of   5.19e+01
26   50   92.6 109 26 W29995   Light chain variable   5.19e+01
27   50   92.6 125 25 W24517   Anti-Factor-IX humani   5.19e+01
28   50   92.6 128 10 R53332   KM-603 light chain.   5.19e+01
29   50   92.6 129 25 W24518   Anti-Factor-IX humani   5.19e+01
30   50   92.6 214 26 W34506   Light chain of full l   5.19e+01
31   50   92.6 214 24 W34504   Light chain of humani   5.19e+01
32   50   92.6 214 24 W27089   Mouse monoclonal anti   5.19e+01
33   50   92.6 228 26 R41704   Vl-Lab-Vh construction   5.19e+01
34   50   92.6 233 6 R30777   pH5z-9.0 humanised mu   5.19e+01
35   50   92.6 235 3 R14695   Vl-Lab-Vh constructio   5.19e+01
36   50   92.6 250 25 W29261   Vl-Lab-Vh constructio   5.19e+01
37   50   92.6 250 23 W24400   Humanised variant of   5.19e+01
38   50   92.6 264 27 W35562   HindIII-EcoR1 insert   5.19e+01
39   50   92.6 355 28 W35125   Single chain antibody   5.19e+01
40   50   92.6 355 28 W35129   R. piplens recombinan   5.19e+01
41   50   92.6 358 28 W35127   R. piplens recombinan   5.19e+01
42   50   92.6 358 28 W35130   R. piplens recombinan   5.19e+01
43   50   92.6 360 28 W35128   R. piplens recombinan   5.19e+01
44   50   92.6 379 28 W35126   HindIII-EcoR1 insert   5.19e+01
45   50   92.6 532 27 W35565   HindIII-EcoR1 insert   5.19e+01
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                            ALIGNMENTS

RESULT     1
ID       W18269  standard; peptide; 95 AA.
AC       W18269;
DT       09-JAN-1998  (first entry)
DE       PrP 81 light chain variable region.
KW       Prion protein; PrP; heavy chain variable region.
KW       light chain variable region; PrP-Sc; pathogen; antibody; scrapie;
KW       central nervous system spongiform encephalopathy; fatal familial insomnia;
KW       transmissible neurodegenerative disease; human; therapy;
KW       bovine spongiform encephalopathy; feline spongiform encephalopathy;
KW       Gerstmann-Strassler-Scheinker Disease; Creutzfeldt-Jakob Disease;
OS       Mus musculus.

FH       Key          Location/Qualifiers
FH
FT       Region        1..9
FT                     /note= "framework region 1"
FT       Misc_difference 3
FT                     /note= "unspecified amino acid"
FT       Region        10..20
FT                     /note= "complementarity determining region 1"
FT       Region        21..35
FT                     /note= "framework region 2"
FT       Region        36..42
FT                     /note= "complementarity determining region 2"
FT       Region        43..74
FT                     /note= "framework region 3"
FT       Region        75..88
FT                     /note= "complementarity determining region 3"
FT       Region        89..95
FT                     /note= "framework region 4"
PN       WO9710505-A1.
PD       20-MAR-1997.
PF       13-SEP-1996;  U14840.
PR       14-SEP-1995;  US-528104.
PA       (REGC ) UNIV CALIFORNIA.
PI       Burton DR, Prusiner SB, Williamson RA;
DR       WPI: 97-202357/18.
PT       New antibodies to the scrapie isoform of prion protein - used for
PT       detection of infectious prion proteins or for treating disease such
PT       as BSE, CJD or scrapie
PS       Example 9; Fig 6; 99pp; English.
CC       W18266-W18285 represent portions of the invention. The
CC       antibodies of the invention are able to bind the scrapie isoform of prion

CC   protein PrP-Sc in situ. Prions are infectious pathogens that cause
CC   central nervous system spongiform encephalopathies in humans and animals.
CC   The scrapie isoform of the prion protein (PrP-Sc) is necessary for both
CC   the transmission and pathogenesis of the transmissible neurodegenerative
CC   diseases of animals and humans. The antibodies can be used in a method of
CC   the invention for detecting human PrP-Sc in a source. The antibodies
CC   specifically bind to prion proteins associated with disease and do not
CC   bind to denatured PrP proteins not associated with disease. They can bind
CC   to prion proteins of a specific species of mammals. They can also have
CC   the ability to neutralise infectious prions. The antibodies can be used
CC   for screening for the presence of prions in products such as
CC   pharmaceuticals, food or cosmetics. They can also be used for prion
CC   neutralisation to purify products, for extraction of prion proteins or
CC   for therapy, for diseases such as bovine spongiform encephalopathy,
CC   Creutzfeldt-Jakob Disease, fatal familial insomnia or
CC   Gerstmann-Strassler-Scheinker Disease, scrapie or feline spongiform
CC   encephalopathies.
SQ   Sequence   95 AA;

Query Match             100.0%;
Best Local Similarity   100.0%;
Matches    9;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       55   sdysltiss  63
              |||||||||
Qy       89   SDYSLTISS  97

RESULT 2
ID   W44122 standard; Protein; 107 AA.
AC   W44122;
DT   05-JUN-1998  (first entry)
DE   Light chain variable region of NR-LU-13 antibody.
KW   antibody; humanised; NR-LU-13; murine; mouse; human; cancer antigen;
KW   antibody; variable region; cancer; diagnosis;
OS   Mus sp.
OS   Mus musculus.
KW   treatment.
FH   Key             Location/Qualifiers
FH
FT   Region          24..34
FT                   /note= "complementarity determining region 1"
FT   Region          50..56
FT                   /note= "complementarity determining region 2"
FT   Region          89..97
FT                   /note= "complementarity determining region 3"

PN   WO9746589-A2.
PD   11-DEC-1997.
PN   06-JUN-1997; U10074.
PD   07-JUN-1996; US-660362.
PS   (NEOR-) NEORX CORP.
PI   Graves SS, Henry AH, Hylarides MD, Mallet RW, Pedersen JT,
PI   Rees AR, Renojm, Searle SMJ;
DR   WPI; 98-042124/04.
DR   N-PSDB; V02198.
PT   Humanised antibody binds same human cancer antigen as antibody
PT   NR-LU-13 - useful for pre-targeting methods, conventional antibody
PT   therapy and immunodiagnosis
PT   Example 1; Fig 2; 100pp; English.
CC   The present sequence is the light chain variable region of the
CC   murine anti-human cancer antigen antibody (Ab) NR-LU-13.
CC   A novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. The
CC   hAb, specifically NRX451, or its conjugates can be used for the
CC   manufacture of a diagnostic or medicament for cancer diagnosis or
CC   treatment. The hAb has reduced immunogenicity and toxicity in
CC   humans, but retains the ability to bind the NR-LU-13 antigen.
SQ   Sequence   107 AA;

Query Match             100.0%;
Best Local Similarity   100.0%;
Matches    9;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       69   sdysltiss  77
              |||||||||
Qy       89   SDYSLTISS  97

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RESULT 3
ID   W27121 standard; Protein; 107 AA.
AC   W27121;
DT   04-JAN-1998  (first entry)
DE   Murine antibody light chain variable region consensus.
KW   Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
KW   human milk fat globule; HMFG; tumour; breast cancer; vaccine.
OS   Mus musculus.
FH   Key             Location/Qualifiers
FH
FT   Region          24..34
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          50..56
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          88..96
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"

PN   WO9722699-A2.
PD   26-JUN-1997.
PF   19-DEC-1996; U20757.
PR   13-DEC-1996; US-575762.
PR   20-DEC-1995; US-575762.
PR   26-JAN-1996; US-591965.
PA   (KENT ) UNIV KENTUCKY.
PI   Chatterjee M, Chatterjee SK, Foon KA;
DR   WPI; 97-341690/31.
PT   Monoclonal anti-idiotype antibody 11D10 - elicits immune response
PT   against human milk fat globule disease associated tumours,
PT   especially breast cancer
PS   Example 2; Fig 26C; 130pp; English.
CC   This polypeptide sequence comprises a consensus sequence of murine
CC   light chain variable regions (VL) selected on the basis of identity
CC   to the VL region (see W27119) of monoclonal anti-idiotype antibody
CC   11D10. The sequences were obtained from a GenBank database
CC   search. A VH consensus (W27122) was also produced. 11D10 has at
CC   least 18 departures from the consensus sequences (7 in the light
CC   chain and 11 in the heavy chain). 8 Occur within CDRs and 10
CC   outside CDRs. 11D10 polypeptides and polynucleotides can be
CC   used in vaccines and pharmaceutical compositions for the treatment
CC   of human milk fat globule-associated diseases such as breast
CC   cancer.
SQ   Sequence   107 AA;

Query Match             100.0%;
Best Local Similarity   100.0%;
Matches    9;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       69   sdysltiss  77
              |||||||||
Qy       89   SDYSLTISS  97

RESULT 4
ID   R21310 standard; Protein; 108 AA.
AC   R21310;
DT   21-MAY-1992  (first entry)
DE   Light chain of M1f clone.
KW   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW   pilus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW   specific binding pairs; replicable genetic display package.
OS   Synthetic.
FH   Key             Location/Qualifiers
FH
FT   region          25..34
FT                   /label= CDR1
FT   region          50..56
FT                   /label= CDR1
FT   region          89..96
FT                   /label= CDR2
FT   region          89..96
FT                   /label= CDR3

PN   WO9201047-A.
PD   23-JAN-1992.

## RESULT 5

```
RESULT 5
ID   R21286 standard; Protein; 108 AA.
AC   R21286;
DT   21-MAY-1992 (first entry)
DE   Murine VL kappa group V chain "a" specific for phOx.
FH   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW   plus; g3p; binding; adsorption; gene VIII; diverse repertoire;
KW   specific binding pairs; replicable genetic display package.
OS   Synthetic.
FH   Key            Location/Qualifiers
FT   binding_site   24..34
FT                  /label= CDR1
FT   binding_site   50..56
FT                  /label= CDR2
FT   binding_site   89..96
FT                  /label= CDR3
FT                  /note= "D-X-G-X-X motif "
PN   WO9201047-A.
PD   23-JAN-1992;
PF   10-JUL-1991; G01134.
PR   10-JUL-1990; GB-015198.
PR   19-OCT-1990; GB-022845.
PR   12-NOV-1990; GB-024503.
PR   06-MAR-1991; GB-004744.
PR   15-MAY-1991; GB-010549.
PA   (CAMB-) CAMBRIDGE ANTIBODY.
PA   (MEDI-) MED RES COUNCIL.
PI   McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
PI   Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI   Winter GP, Bonnert TP;
DR   WPI; 92-056862/07.
PT   Producing members of specific binding pairs - by expression in
PT   recombinant host cells with a secreting replicable genetic
PT   display package.
PS   Example 46; Fig 52; 109pp; English.
CC   The sequence is the light chain of clone MIF encoding an scFv frag-
CC   ment specific for both hen and turkey egg lysozyme (HEL and TEL).
CC   The DNA encoding the chain was amplified from a cDNA library prepd.
CC   from the spleen of an unimmunised mouse. The corresponding heavy
CC   chain was also amplified from an existing construct, pSW1-VHD1.3
CC   (Ward et al, 1989). The two fragments were assembled via a linker
CC   to prepare an scFv construct which was ligated into the fdCAT2
CC   vector for expression on the surface of Id bacteriophage. In this
CC   way, the VL domain was replaced by a library of VL domains to allow
CC   for selection of a broader range of antibody specificities. Several
CC   clones were isolated which bound to TEL (the parent antibody D1.3
CC   binds exclusively to HEL). The sequences of the light chains of
CC   two of these clones, MF1 and M21 are given in R21310 and R21311
CC   respectively. The D1.3 light chain is given in R21309.
CC   See also R21260-307, 309-312, R22450, R22565, R22567-81.
SQ   Sequence 108 AA;
```

Query Match   100.0%;   Score 54;   DB 4;   Length 108;
Best Local Similarity 100.0%;   Pred. No. 1.90e+01;
Matches   9;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   69 sdysltiss 77
        |||||||||
Db   89 SDYSLTISS 97
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RESULT 6

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RESULT 6
ID   W18271 standard; peptide; 109 AA.
AC   W18271;
DT   09-JAN-1998 (first entry)
DE   PrP 37 light chain variable region.
KW   Prion protein; PrP; heavy chain variable region; antibody; scrapie;
KW   light chain variable region; PrP-Sc; pathogen; fatal familial insomnia;
KW   central nervous system spongiform encephalopathy; human; therapy;
KW   transmissible neurodegenerative disease; Creutzfeldt-Jakob Disease;
KW   bovine spongiform encephalopathy; feline spongiform encephalopathy;
OS   Serstmann-Strassler-Scheinker Disease.
OS   Mus musculus.
FH   Key        Location/Qualifiers
FT   Region     1..23
FT              /note= "framework region 1"
FT   Region     24..34
FT              /note= "complementarity determining region 1"
FT   Region     35..49
FT              /note= "framework region 2"
FT   Region     50..56
FT              /note= "complementarity determining region 2"
FT   Region     57..88
FT              /note= "framework region 3"
FT   Region     89..97
FT              /note= "complementarity determining region 3"
FT   Region     98..109
FT              /note= "framework region 4"
PN   WO9710505-A1.
PD   20-MAR-1997;
PF   13-SEP-1996; U14840.
PR   14-SEP-1995; US-528104.
PA   (REGC ) UNIV CALIFORNIA.
PI   Burton DR, Prusiner SB, Williamson RA;
DR   WPI; 97-202357/18.
PT   New antibodies to the scrapie isoform of prion protein - used for
PT   detection of infectious prion proteins or for treating disease such
PT   producing members of specific binding pairs - by expression in
PT   recombinant host cells with a secreting replicable genetic
PT   display package.
PS   Example 21; Fig 24; 209pp; English.
CC   The VK sequence is one of seven (R21286-92) found to be expressed
CC   from a single chain Fv library from an immunised mouse. The libra-
CC   ry produces a diverse repertoire of antibody fragments specific for
CC   2-phenyl-5-oxazolone (phOx). It was prepd. using cDNA generated
CC   from mRNA from mice immunised with phOx coupled to chicked serum
CC   albumin. The VH and VL kappa sequences were separately amplified
CC   by PCR (see Q2347-84) and ligated into fdCAT2 (see Q23463) for ex-
CC   pression on the phage surface as fusions with gene III. The result-
CC   ing library of clones was diverse revealing twenty three different VH
CC   clones were sequenced revealing eight different VH genes (A-H) (see
CC   R21264-71) in a variety of pairings with the seven different Vk
CC   genes (a-g). Of the twenty three clones sequenced, three were of
CC   type "a", and were "ox-like" genes. (See Berek et al, Nature 316
CC   412-418, 1985). They contain the DXGXX motif in CDR3, the central
CC   Gly of which is needed to create a cavity for phOx. Most of the
CC   clones were Vk-d combinations. The Kd of VH-B/Vk-d for phOx-GABA
CC   was 10 nM. Only two other combinations (of eleven tested) were
CC   found to have higher values. This suggests that phage bearing scFv
CC   fragments having weak affinities can be selected with antigen, pro-
CC   bably due to the avidity of the multiple antibody heads on the
CC   phage.
CC   See also R21260-307, 309-311; R22450, 565-581.
SQ   Sequence 108 AA;
```

Query Match   100.0%;   Score 54;   DB 4;   Length 108;
Best Local Similarity 100.0%;   Pred. No. 1.90e+01;
Matches   9;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   69 sdysltiss 77
        |||||||||
Db   89 SDYSLTISS 97
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PT   as BSE, CJD or scrapie
PS   Example 9; Fig 6; 99pp; English.
PT   W18266-W18285 represent portions of the antibodies of the invention. The
CC   antibodies of the invention are able to bind the scrapie isoform of prion
CC   protein PrP-Sc in situ. Prions are infectious pathogens that cause
CC   central nervous system spongiform encephalopathies in humans and animals,
CC   The scrapie isoform of the prion protein (PrP-Sc) is necessary for both
CC   the transmission and pathogenesis of the transmissible neurodegenerative
CC   diseases of animals and humans. The antibodies can be used in a method of
CC   the invention for detecting PrP-Sc in a source. The antibodies
CC   specifically bind to prion proteins associated with disease and do not
CC   bind to denatured PrP proteins not associated with disease. The antibodies
CC   to prion proteins of a specific species of mammals. They can bind
CC   the ability to neutralise infectious prions. The antibodies can also have
CC   for screening for the presence of prions in products such as
CC   pharmaceuticals, food or cosmetics. They can also be used for prion
CC   neutralisation to purify products, for extraction of prion proteins or
CC   for therapy, for diseases such as bovine spongiform encephalopathy,
CC   Creutzfeldt-Jakob Disease, fatal familial Insomnia or
CC   Gerstmann-Strassler-Scheinker Disease, scrapie or feline spongiform
SQ   encephalopathies.
SQ   Sequence 109 AA;

Query Match   100.0%; Score 54; DB 25; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.90e+01;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   69 sdysltss 77
         |||||||||
Qy   89 SDYSLTSS 97

RESULT   7
ID   R52030 standard; Protein; 109 AA.
AC   R52030;
DT   26-SEP-1996 (first entry)
DE   Light chain variable region of murine antibody glb2.
KW   antibody; humanised; murine; human; heavy chain; light; variable;
KW   framework region; complementarity determining region; light; reshaping;
KW   modelling; surface residue; modify.
OS   Mus sp.
FH   Key   Location/Qualifiers
FT   region   1..23
FT   /label= framework_region_1
FT   /note= "FR 1"
FT   region   24..34
FT   /label= complementarity_determining_region_1
FT   /note= "CDR 1"
FT   region   35..49
FT   /label= FR_2
FT   region   50..56
FT   /label= CDR_2
FT   region   57..88
FT   /label= FR_3
FT   region   89..97
FT   /label= CDR_3
FT   region   98..109
FT   /label= FR_4

Db   69 sdysltss 77
         |||||||||
Qy   89 SDYSLTSS 97

PN   EP-592106-A1.
PD   13-APR-1994.
PF   07-SEP-1993; 307051.
PR   09-SEP-1992; US-942245.
PA   (PEDE/) PEDERSEN J T.
PA   (IMMU-) IMMUNOGEN INC.
PI   Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
DR   WPI; 94-120230/15.
PT   Method of resurfacing of rodent antibodies to produce humanised
PT   antibody forms - for producing non-human antibodies with improved
PT   therapeutic efficiency by presenting human surface on V-region
PA   Example 1; Fig 3A; 230pp; English.
PS   The present sequence is that of the light chain variable (LC VR) region
PT   of murine antibody glb2. This sequence was aligned with 11 other known
CC   antibody LC VRs and a set of framework positions of surface exposed amino
CC   acid residues was determined. This information can be used in a method to
CC   determine how to modify a rodent antibody or fragment by resurfacing in
CC   order to produce a humanised rodent antibody. Residues (determined from
CC   alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86,
CC   87, 101, 105, 106 and 108 are likely to be exposed on the surface of the
CC   light chain variable region. The residues of the murine LC VR region of
CC   antibody glb2 at positions 3, 9, 18, 46, 63, 66, 73, and 101 may be
CC   compared with the equivalent surface positions of known human antibody
CC   LC VRs. If they differ, the murine residues may be modified to the human
CC   residues. The murine position residues may also be compared with the
CC   equivalent human residue positions and vice versa. However the residues of
CC   positions appear to be conserved.

Query Match   100.0%; Score 54; DB 18; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.90e+01;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   69 sdysltss 77
         |||||||||
Qy   89 SDYSLTSS 97

RESULT   8
ID   W22537 standard; Protein; 129 AA.
AC   W22537;
DT   03-NOV-1997 (first entry)
DE   Murine anti-human class II monoclonal antibody 44H104.
KW   Antibody; light chain; variable region; hybridoma cell line 44H104;
KW   immune response; enhance; stimulate; vaccine; immunodiagnosis;
KW   antigen delivery.
OS   Mus musculus.
PN   WO9640941-A1.
PD   19-DEC-1996.
PR   07-JUN-1996; US-483576.
PR   07-JUN-1995; CA0400.
PA   (CONN-) CONNAUGHT LAB LTD.
PI   Anand NN, Barber BH, Caterini JE, Cates GC, Klein MH;
DR   WPI; 97-077271/07.
DR   N-PSDB; T77851.
PT   Recombinant conjugate antibody mol., modified for delivering an
PT   antigen - elicits enhanced immune response without the use of
PT   adjuvant to generate antibodies which are useful in vaccines or
PT   immuno:diagnosis
PS   Example 1; Fig 1A; 64pp; English.
CC   Novel recombinant conjugate antibody molecules comprise a monoclonal
CC   antibody specific for a surface structure of antigen presenting
CC   cells (APC), genetically modified to contain at least one antigen
CC   exclusively at one or more preselected sites. The conjugate is capable
CC   of delivering the antigen to APC and eliciting an immune response to
CC   the antigen. The new conjugates are useful as vaccines and are able
CC   to elicit an enhanced immune response without the use of an adjuvant.
CC   In a specific example, a conjugate was constructed using the murine
CC   anti-human class II monoclonal antibody secreted by the murine
CC   44H104. The peptide CLTB36 was chosen as antigen; it consists of
CC   a tandemly linked T and B cell epitope derived from HIV MN strain.
CC   The present sequence represents the light chain variable region
CC   from 44H104 which was used in the preparation of a conjugate with
CC   antigen CLTB36.
SQ   Sequence 129 AA;

Query Match   100.0%; Score 54; DB 24; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.90e+01;
Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Db   91 sdysltss 99
         |||||||||
Qy   89 SDYSLTSS 97

RESULT   9
ID   W27119 standard; Protein; 145 AA.
AC   W27119;
DT   04-JAN-1998 (first entry)
DE   Murine monoclonal anti-idiotype antibody 11D10 VL region.
KW   Monoclonal antibody 11D10; anti-idiotype antibody; tumour;
KW   human milk fat globule; HMFG; tumour; breast cancer; vaccine.

Column 1

```
OS   Mus musculus.
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Sig_peptide
FT   Protein         21..145
FT                   /label= Mat_protein
FT   Region          21..43
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          109..117
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Region          118..127
FT                   /label= FR1
FT                   /note= "framework region 4"
PN   WO9722699-A2.
PD   26-JUN-1997.
PF   19-DEC-1996; U20757.
PF   13-DEC-1996; US-575762.
PR   20-DEC-1995; US-575762.
PR   20-DEC-1995; US-591965.
PR   26-JAN-1996; US-591965.
PA   (KENT ) UNIV KENTUCKY.
PI   Chatterjee M, Chatterjee SK, Foon KA;
DR   WPI; 97-341690/31.
DR   N-PSDB; T85149.
PT   Monoclonal anti-idiotype antibody 11D10 - elicits immune response
PT   against human milk fat globule disease associated tumours,
PT   especially breast cancer
PS   Claim 9; Page 94; 130pp; English.
CC   This polypeptide sequence comprises the light chain variable region
CC   (VL) of monoclonal anti-idiotype antibody 11D10 produced by
CC   hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
CC   naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype
CC   response. It elicits an immune response against a specific epitope
CC   of a high mol.wt. mucin of human milk fat globule (HMFG). It
CC   induces an immunological response to HMFG in mice, rabbits, monkeys
CC   and patients with advanced HMFG-associated tumours. Pharmaceutical
CC   compositions and vaccines comprising 11D10, 11D10 polypeptides
CC   and/or 11D10 polynucleotides (see also T85149-50) are claimed.
CC   Also claimed are diagnostic kits and methods of using 11D10, 11D10
CC   polypeptides and/or 11D10 polynucleotides, including methods of
CC   treating HMFG-associated tumours. 11D10 is also used in a claimed
CC   method of palliating HMFG-associated disease and in claimed kits to
CC   detect or quantify anti-HMFG antibody.
SQ   Sequence 145 AA;

Query Match             100.0%;  Score 54;  DB 25;  Length 145;
Best Local Similarity   100.0%;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db         89  sdysltiss  97
               |||||||||
Qy         89  SDYSLTISS  97
```

```
RESULT 10
ID   P30251 standard; peptide; 146 AA.
AC   P30251;
DT   25-MAY-1992 (first entry)
DE   Sequence of the leader, variable region and first 16 AAs of
DE   the constant region of the kappa-chain (light chain) of MOPC41.
```

Column 2

```
KW   Diagnosis; therapy; Immunoglobulin.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   region          1..22
FT                   /label= leader
FT   region          23..130
FT                   /label= variable
FT   region          131..146
FT                   /label= constant
PN   EP--88994-A.
PD   21-SEP-1983.
PF   10-MAR-1983; 001655.
PF   15-MAR-1982; US-358414.
PR   05-DEC-1983; US-558551.
PA   (SCHE ) SCHERING CORP.
PA   (DNAX-) DNAX RES INST.
PI   Moore KW, Zaffaroni A;
DR   WPI; 83-772290/39.
DR   N-PSDB; N30165.
PT   Transformed expression vectors or plasmid(s) - with double
PT   stranded DNA sequence coding only for desired part of polypeptide
PT   chain
PS   Example; Page 40-41; 68pp; English.
CC   The pref. vector or plasmid of the invention has a double-stranded
CC   DNA seq. coding for a variable region of a light or heavy chain of
CC   IgG, or for a variable region of a light or heavy chain of an
CC   immunoglobulin specific for an enzyme or surface protein. The
CC   sequence esp. codes for a variable region of a light chain having 95-
CC   115 AAs or for a variable region of a heavy chain having 110-125 AAs
CC   esp. including the D region of the heavy chain.
SQ   Sequence 146 AA;

Query Match             100.0%;  Score 54;  DB 4;  Length 146;
Best Local Similarity   100.0%;  Pred. No. 1.90e+01;
Matches    9;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db         91  sdysltiss  99
               |||||||||
Qy         89  SDYSLTISS  97
```

```
RESULT 11
ID   W02280 standard; Protein; 243 AA.
AC   W02280;
DT   29-OCT-1996 (first entry)
DE   520C9 anti-c-erbB-2 two single chain Fv construct.
```

Column 3

```
KW   520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sFV;
KW   construct; polypeptide linker; C-terminal amino acid sequence;
KW   In vivo imaging; drug targeting experiment; homodimer;
KW   increased; binding avidity; tissue retention time.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         118..133
FT                   /label= linker
PN   US5534254-A.
PD   09-JUL-1996.
PF   06-FEB-1992; 831967.
PF   06-FEB-1992; US-831967.
PR   07-OCT-1993; US-133804.
PA   (CHIR ) CHIRON CORP.
PA   (CREA-) CREATIVE BIOMOLECULES INC.
PI   Houston LL, Huston JS, Oppermann H, Ring DB;
DR   WPI; 96-333394/33.
DR   N-PSDB; T36880.
PT   Compsns. contg. antigen-targetting antibody fragment constructs -
PT   comprising dimer of single-chain Fv fragments
PS   Example 1; Columns 33-36; 30pp; English.
CC   Example 1; Columns 33-36. 30pp; English.
CC   Variable heavy (VH) and variable light (VL) genes were cloned from
CC   a 520C9 hybridoma cDNA library, using probes directed toward the
CC   antibody constant and joining regions. A two single chain Fv (sFV)
CC   gene was constructed by connecting the VH and VL genes with a
CC   Ser rich polypeptide linker. The resulting 520C9 two sFv gene,
CC   which encodes the present sequence, was inserted into an expression
```

CC vector, transformed into E. coli, and protein expression induced by
CC the addn. of IPTG to the culture medium.
CC A compsn. comprising a carrier and the 2 sFv protein prod. can be
CC used for in vivo imaging, and drug targeting experiments. The
CC 2 sFv protein prod. is a homodimer, in which both fragments target
CC the same antigen, therefore giving greater binding avidity and
CC longer tissue retention times, compared to individual sFv protein
CC prod. fragments.
SQ Sequence 243 AA;

Query Match 100.0%; Score 54; DB 18; Length 243;
Best Local Similarity 100.0%;
Matches 9; Conservative 0; Pred. No. 1.90e+01; Mismatches 0; Indels 0; Gaps 0;

```
Qy  202 sdysltiss 210
        |||||||||
Db   89 SDYSLTISS 97
```

RESULT 12
ID R39569 standard; Protein; 246 AA.
AC R39569;
DT 07-FEB-1994 (first entry)
DE Sequence of 520C9 sFv protein.
KW biosynthetic single polypeptide; VH-VL heterodimer; Immunoglobulin; Ig;
OS Synthetic.
PN WO9316185-A.
PD 19-AUG-1993.
PF 05-FEB-1993; U01055.
PR 06-FEB-1992; US-831967.
PA (CETU) CETUS ONCOLOGY CORP.
PA (CREA) CREATIVE BIOMOLECULES INC.
PI Houston LL, Huston JS, Oppermann H, Ring DB;
DR WPI; 93-272889/34.
DR N-PSDB; Q46084.
PT New single chain Fv polypeptide binding to C-erbB-2 tumour
PT antigen - for imaging or treating breast or ovarian cancer etc.
PS Claim 4; pages 60-61; 87pp; English.
CC c-erbB-2 refers to a protein antigen expressed on the surface of
CC tumour cells, such as breast and ovarian tumour cells, which is an
CC acidic glycoprotein having an isoelectric
CC pt. of about 5.3 (see Q46083, R39568). A single chain Fv (sFv)
CC is a covalently linked VH- and VL- heterodimer which is expressed from
CC a gene fusion including VH- and VL- encoding genes connected by
CC a peptide-encoding linker. Such linker sequences are set forth in
CC AA residues 116-135 in R39569, which includes part of the 16 AA
CC linker sequences in R39572. Using Q46084 for the 520C9 monoclonal
CC antibody, a single chain polypeptide can be produced having a
CC binding affinity for a c-erbB-2 related antigen. 'x' in R39569
CC refers to the location of a stop codon in Q46084.
SQ Sequence 246 AA;

Query Match 100.0%; Score 54; DB 8; Length 246;
Best Local Similarity 100.0%;
Matches 9; Conservative 0; Pred. No. 1.90e+01; Mismatches 0; Indels 0; Gaps 0;

```
Qy  202 sdysltiss 210
        |||||||||
Db   89 SDYSLTISS 97
```

RESULT 13
ID R39571 standard; Protein; 534 AA.
AC R39571;
DT 07-FEB-1994 (first entry)
DE Sequence of G-FIT.
KW Tumour antigen; c-erbB-2; G-FIT.
OS Synthetic.
PN WO9316185-A.
PD 19-AUG-1993.
PF 05-FEB-1993; U01055.
PR 06-FEB-1992; US-831967.
PA (CETU) CETUS ONCOLOGY CORP.
PA (CREA) CREATIVE BIOMOLECULES INC.
PI Houston LL, Huston JS, Oppermann H, Ring DB;
DR WPI; 93-272889/34.
DR N-PSDB; Q46086.
PT New single chain Fv polypeptide binding to C-erbB-2 tumour
PT antigen - for imaging or treating breast or ovarian cancer etc.
PS Example; pages 65-68; 87pp; English.
CC New single chain Fv polypeptide binding to C-erbB-2 tumour
CC antigen expressed on the surface of tumour cells, which is an isoelectric
CC c-erbB-2 refers to a protein antigen expressed on the surface of
CC tumour cells, such as breast and ovarian tumour cells, which is an
CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
CC pt. of about 5.3 (see Q46083, R39568).
SQ Sequence 534 AA;

Query Match 100.0%; Score 54; DB 8; Length 534;
Best Local Similarity 100.0%;
Matches 9; Conservative 0; Pred. No. 1.90e+01; Mismatches 0; Indels 0; Gaps 0;

```
Qy  493 sdysltiss 501
        |||||||||
Db   89 SDYSLTISS 97
```

RESULT 14
ID W44123 standard; Protein; 107 AA.
AC W44123;
DT 05-JUN-1998 (first entry)
DE Light chain variable region of humanised NR-LU-13 antibody NRX451.
KW Light chain; variable region; murine; mouse; human; cancer antigen;
KW antibody; humanised; NR-LU-13; NRX451; cancer; diagnosis;
KW treatment.
OS Mus sp.
OS Synthetic.
PN WO9746589-A2.
PD 11-DEC-1997.
PF 06-JUN-1997; U10074.
PR 07-JUN-1996; US-660362.
PA (NEOR-) NEORX CORP.
PI Graves SS, Henry AH, Hylarides MD, Mallet RW, Pedersen JT,
PI Rees-AR, Renojm, Searle SMJ;
DR WPI; 98-042124/04.
PT A novel humanised anti-human cancer antigen antibody (Ab) NR-LU-13,
PT NRX451.
PT Humanised antibody binds same human cancer antigen as antibody
PT NR-LU-13 - useful for pre-targeting methods, conventional antibody
PT therapy and immunodiagnosis
PS Example 1; Fig 3; 100pp; English.
CC The present sequence is the light chain variable region of the
CC humanised murine anti-human cancer antigen antibody NR-LU-13,
CC NRX451.
CC A novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. The
CC hAb, specifically NRX451, or its conjugates can be used for the
CC manufacture of a diagnostic or medicament for cancer diagnosis or
CC treatment. The hAb has reduced immunogenicity and toxicity in
CC humans, but retains the ability to bind the NR-LU-13 antigen.
SQ Sequence 107 AA;

FH Key   Location/Qualifiers
FT Region   24..34
FT   /note= "complementarity determining region 1"
FT Region   50..56
FT   /note= "complementarity determining region 2"
FT Region   89..97
FT   /note= "complementarity determining region 3"

Query Match 96.3%; Score 52; DB 29; Length 107;
Best Local Similarity 88.9%;
Matches 8; Conservative 1; Pred. No. 3.15e+01; Mismatches 0; Indels 0; Gaps 0;

```
Qy   69 sdysltiss 77
        ||:||||||
Db   89 SDYSLTISS 97
```

RESULT 15
ID R32125 standard; Protein; 127 AA.

```
AC   R32125;
DT   02-JUN-1993 (first entry)
DE   Anti-IL2R alpha antibody 179 light chain variable region.
KW   immunosuppression; tissue transplantation; graft; L chain; V region;
KW   T-helper cell inhibition; transplant rejection; MAb;
KW   interleukin-2 receptor.
FH   Key             Location/Qualifiers
FT   peptide         1..20
FT                   /label= signal
FT   region          21..115
FT                   /label= Variable
FT   region          116..127
FT                   /label= J1
PN   DE4143214-A.
PD   28-JAN-1993.
PF   30-DEC-1991; 143214.
PR   25-JUL-1991; DE-124759.
PR   30-DEC-1991; DE-143214.
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
PA   Kaluza B, Riethmueller G, Scheuer W, Weidle U;
DR   WPI; 93-037582/05.
DR   N-PSDB; Q36611.
PT   Synergistic antibody compsn. for use as immunosuppressant -
PT   comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
PT   alpha- or anti-IL2R beta antibodies
PS   Claim 6; Page 13; 18pp; German.
CC   This sequence is the light chain variable region of a preferred
CC   anti-IL2R alpha monoclonal antibody for use in the claimed
CC   synergistic composition. MAb 179 is deposited as clone 3G10/179
CC   (ECACC 90071905). The anti-IL2R alpha antibody is used with at least
CC   one anti-CD4 antibody. Individually the antibodies are strongly
CC   inhibiting and when used together their immunosuppressive properties
CC   are improved; they synergistically inhibit T-helper cell
CC   proliferation to effectively inhibit transplant rejection at low
CC   doses without significantly reducing the general immune response.
CC   See Q36607-Q36616.
SQ   Sequence        127 AA;
```

```
Query Match        96.3%;   Score 52;  DB 6;  Length 127;
Best Local Similarity   88.9%;   Pred. No. 3.15e+01;
Matches     8;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Db         89  adyslitss 97
               :||||||||
Qy         89  SDYSLTISS 97
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MPSRCH (TM)

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

run on: Tue Apr 20 13:57:31 1999, MasPar time 2.58 Seconds
              ---177.019 Million cell updates/sec

Tabular output not generated.

Title:	>US-08-836-455-2
Description:	(50-66) from US08364555.pep (2 of 3)
Perfect Score:	131
Sequence:	1 GINLHWLQOEPDGTIKR 17
Scoring table:	PAM 150
	Gap 11
Searched:	74019 seqs, 26840295 residues
Post-processing:	Minimum Match 0%
	Listing first 45 summaries
Database:	swiss-prot35
	1:swissprot
Statistics:	Mean 28.762; Variance 43.396; scale 0.663

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	Match DB	ID	Description	Pred. No.
1	110	84.0	130	1	KV5G_MOUSE	IG KAPPA CHAIN PRECURS	1.23e-09
2	78	59.5	108	1	KV5J_MOUSE	IG KAPPA CHAIN V-V REG	4.59e-03
3	76	58.0	108	1	KV5M_MOUSE	IG KAPPA CHAIN V-V REG	1.10e-02
4	76	58.0	108	1	KV5U_MOUSE	IG KAPPA CHAIN V-V REG	1.10e-02
5	76	58.0	108	1	KV5L_MOUSE	IG KAPPA CHAIN V-V REG	1.10e-02
6	76	58.0	108	1	KV5K_MOUSE	IG KAPPA CHAIN V-V REG	1.10e-02
7	76	58.0	108	1	KV5N_MOUSE	IG KAPPA CHAIN V-V REG	1.10e-02
8	70	53.4	108	1	KV5O_MOUSE	IG KAPPA CHAIN V-V REG	1.10e-02
9	67	51.1	447	1	YCAJ_ECOLI	HYPOTHETICAL 49.6 KD P	4.70e-01
10	67	51.1	570	1	HEMA_IAHC6	HEMAGGLUTININ PRECURSO	4.70e-01
11	67	51.1	570	1	HEMA_IAHP9	HEMAGGLUTININ PRECURSO	4.70e-01
12	67	50.4	346	1	UFO2_MANES	FLAVONOL 3-O-GLUCOSYLT	7.02e-01
13	66	50.4	365	1	VSI3_REOVL	SIGMA 3 PROTEIN (MAJOR	7.02e-01
14	66	50.4	560	1	HEMA_IATKR	HEMAGGLUTININ PRECURSO	7.02e-01
15	66	49.6	563	1	HEMA_IAFPR	HEMAGGLUTININ PRECURSO	1.04e+00
16	64	48.9	108	1	KV5S_MOUSE	IG KAPPA CHAIN V-V REG	1.55e+00
17	64	48.9	108	1	KV5T_MOUSE	IG KAPPA CHAIN V-V REG	1.55e+00
18	63	48.1	108	1	KV5Q_MOUSE	IG KAPPA CHAIN V-V REG	2.28e+00
19	63	48.1	108	1	KV5R_MOUSE	IG KAPPA CHAIN V-V REG	2.28e+00
20	63	48.1	255	1	YS84_CAEEL	HYPOTHETICAL 29.8 KD P	2.28e+00
21	63	48.1	320	1	STBA_ECOLI	PROTEIN STBA (PARA LOC	2.28e+00
22	62	47.3	406	1	WCAL_ECOLI	PUTATIVE COLANIC ACID	3.35e+00
23	61	46.6	263	1	COQ4_CAEEL	UBIQUINONE BIOSYNTHESI	4.90e+00
24	61	46.6	374	1	SMF_ECOLI	SMF PROTEIN.	4.90e+00
25	61	46.6	475	1	YBES_ECOLI	HYPOTHETICAL 55.3 KD P	4.90e+00
26	61	46.6	563	1	HEMA_IASTA	HEMAGGLUTININ PRECURSO	4.90e+00
27	61	46.6	563	1	HEMA_IACKV	HEMAGGLUTININ PRECURSO	4.90e+00
28	61	46.6	780	1	YCAI_ECOLI	HYPOTHETICAL 87.3 KD P	4.90e+00
29	59	45.0	109	1	CYPC_STRHA	PUTATIVE POLYKETIDE CY	1.03e+01
30	59	45.0	111	1	KV3E_MOUSE	IG KAPPA CHAIN V-III R	1.03e+01
31	59	45.0	119	1	Y128_SYNP6	HYPOTHETICAL 12.8 KD P	1.03e+01
32	59	45.0	120	1	HV3U_HUMAN	IG HEAVY CHAIN V-III R	1.03e+01
33	59	45.0	406	1	WCAL_SALTY	PUTATIVE COLANIC ACID	1.03e+01
34	59	45.0	516	1	Y4NM_RHISN	HYPOTHETICAL 57.3 KD P	1.03e+01
35	59	45.0	570	1	HEMA_IAHHN	HEMAGGLUTININ PRECURSO	1.03e+01
36	59	45.0	570	1	HEMA_IAHDE	HEMAGGLUTININ PRECURSO	1.03e+01
37	59	45.0	570	1	HEMA_IAHCD	HEMAGGLUTININ PRECURSO	1.03e+01
38	59	45.0	986	1	EPA4_HUMAN	EPHRIN TYPE-A RECEPTOR	1.03e+01
39	59	45.0	986	1	EPA4_CHICK	EPHRIN TYPE-A RECEPTOR	1.03e+01
40	59	45.0	986	1	EPA4_MOUSE	EPHRIN TYPE-A RECEPTOR	1.03e+01
41	58	44.3	221	1	GSHE_RAT	EPIDIDYMAL SECRETORY G	1.49e+01
42	58	44.3	570	1	HEMA_IAHSW	HEMAGGLUTININ PRECURSO	1.49e+01
43	58	44.3	570	1	HEMA_IAHSP	HEMAGGLUTININ PRECURSO	1.49e+01
44	58	44.3	570	1	HEMA_IAHLO	HEMAGGLUTININ PRECURSO	1.49e+01
45	58	44.3	2329	1	YLJ6_CAEEL	HYPOTHETICAL 272.0 KD	1.49e+01

ALIGNMENTS

```
RESULT 1
ID   KV5G_MOUSE          STANDARD;      PRT;     130 AA.
AC   P01639; P01640;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 41).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 79221900.
RA   SEIDMAN J.G.; MAX E.E., LEDER P.;
RL   NATURE 280:370-375(1979).
RN   [2]
RP   SEQUENCE OF 1-33.
RX   MEDLINE; 77148916.
RA   BURSTEIN Y.; SCHECHTER I.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 74:716-720(1977).
RN   [3]
RP   SEQUENCE OF 23-130.
RX   MEDLINE; 67056897.
RA   GRAY W.R.; DREYER W.J.; HOOD L.;
RL   SCIENCE 155:465-467(1967).
CC   -!- THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE SYSTEM DIRECTED BY
CC       MRNA ISOLATED FROM MYELOMA POLYSOMES.
CC   -!- THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01922; KVMSM4.
DR   HSSP; P01607; 6FAB.
KW   IMMUNOGLOBULIN V REGION; SIGNAL; BENCE-JONES PROTEIN.
FT   SIGNAL         1     22
FT   CHAIN         23    116       IG KAPPA CHAIN V-V REGION (MOPC 41).
FT   DOMAIN        23     45       FRAMEWORK 1.
FT   DOMAIN        46     56       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        57     71       FRAMEWORK 2.
FT   DOMAIN        72     78       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        79    110       FRAMEWORK 3.
FT   DOMAIN       111    119       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       120    129       FRAMEWORK 4.
FT   VARIANT        1      2       MISSING (IN 25% OF THE MOLECULES).
FT   DISULFID      45    110       BY SIMILARITY.
FT   NON_TER      130    130
SQ   SEQUENCE   130 AA;   14311 MW;   E77D75A2 CRC32;
```

Query Match   84.0%;   Score 110; DB 1; Length 130;
Best Local Similarity   82.4%;   Pred. No. 1.23e-09;

RESULT 2

Matches   14;   Conservative   2;   Mismatches   1;   Indels   0;   Gaps   0;

Db   52   GSSLNWLQQEPDGTIKR 68
              |:|:|||||||||||||
Qy   50   GINLHWLQQEPDGTIKR 66

ID   KV5J_MOUSE   STANDARD;   PRT;   108 AA.
AC   P01643;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (MOPC 173).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RA   SCHIFF C., FOUGEREAU M.;
RL   EUR. J. BIOCHEM. 59:525-537(1975).
CC   -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01926; KVMS73.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   108   FRAMEWORK 4.
FT   DISULFID   23   88   BY SIMILARITY.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA;   11819 MW;   EA186054 CRC32;

Query Match
Best Local Similarity   59.5%;   Score 78;   DB 1;   Length 108;
Matches   10;   Conservative   2;   Mismatches   4;   Indels   0;   Gaps   0;

Db   30   GNYLBWYQQKPDGTVK 45
              |:|| ||||||:|
Qy   50   GINLHWLQQEPDGTIK 65

JLT   3

ID   KV5M_MOUSE   STANDARD;   PRT;   108 AA.
AC   P01646;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 12366).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
PIR; A01927; KVMSAR.
HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   108   FRAMEWORK 4.

RESULT 4

ID   KV5U_MOUSE   STANDARD;   PRT;   108 AA.
AC   P04946;
DT   13-AUG-1987 (REL. 05, CREATED)
DT   13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (NQ5-89.4).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RX   MEDLINE; 83271467.
RA   KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;
RL   NATURE 304:320-324(1983).
CC   -!- ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
DR   EMBL; K00745; G196455; -.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; HYBRIDOMA.
FT   DOMAIN   1   23   FRAMEWORK 1.
FT   DOMAIN   24   34   COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN   35   49   FRAMEWORK 2.
FT   DOMAIN   50   56   COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN   57   88   FRAMEWORK 3.
FT   DOMAIN   89   97   COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN   98   107   FRAMEWORK 4.
FT   DISULFID   23   88   BY SIMILARITY.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA;   11866 MW;   D396F142 CRC32;

Query Match
Best Local Similarity   58.0%;   Score 76;   DB 1;   Length 108;
Matches   9;   Conservative   2;   Mismatches   2;   Indels   0;   Gaps   0;

Db   33   LNWYQQKPDGTVK 45
              |:| || |||||:|
Qy   53   LHWLQQEPDGTIK 65

FT   DISULFID   23   88   BY SIMILARITY.
FT   NON_TER   108   108
SQ   SEQUENCE   108 AA;   11989 MW;   23B8BB67 CRC32;

Query Match
Best Local Similarity   58.0%;   Score 76;   DB 1;   Length 108;
Matches   9;   Conservative   2;   Mismatches   2;   Indels   0;   Gaps   0;

Db   33   LNWYQQKPDGTVK 45
              |:| || |||||:|
Qy   53   LHWLQQEPDGTIK 65

RESULT 5

ID   KV5L_MOUSE   STANDARD;   PRT;   108 AA.
AC   P01645;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 93G7).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
PIR; A01927; KVMSAR.
HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN   1   23   FRAMEWORK 1.

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FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    108       FRAMEWORK 4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE    108 AA;   11954 MW;   A203E130 CRC32;

Query Match              58.0%;  Score 76;   DB 1;  Length 108;
Best Local Similarity    69.2%;  Pred. No. 1.10e-02;
Matches    9;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   53 LHWLQQEPDGTIK 65
        |:| || |||||:|
Db   33 LNWYQQKPDGTVK 45


RESULT 6
ID   KV5K_MOUSE   STANDARD;      PRT;   108 AA.
AC   P01644;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP R16.7).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RX   STRAIN=A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
CC   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN         1     23       FRAMEWORK 1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    108       FRAMEWORK 4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE    108 AA;   11910 MW;   64A62905 CRC32;

Query Match              58.0%;  Score 76;   DB 1;  Length 108;
Best Local Similarity    69.2%;  Pred. No. 1.10e-02;
Matches    9;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   53 LHWLQQEPDGTIK 65
        |:| || |||||:|
Db   33 LNWYQQKPDGTVK 45


RESULT 7
ID   KV5N_MOUSE   STANDARD;      PRT;   108 AA.
AC   P01647;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 124E1).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE; 82150934.
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RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
CC   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN         1     23       FRAMEWORK 1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    108       FRAMEWORK 4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE    108 AA;   11961 MW;   5B067780 CRC32;

Query Match              58.0%;  Score 76;   DB 1;  Length 108;
Best Local Similarity    69.2%;  Pred. No. 1.10e-02;
Matches    9;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   53 LHWLQQEPDGTIK 65
        |:| || |||||:|
Db   33 LNWYQQKPDGTVK 45


RESULT 8
ID   KV5O_MOUSE   STANDARD;      PRT;   108 AA.
AC   P01648;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE   IG KAPPA CHAIN V-V REGION (HP 91A3).
OS   MUS MUSCULUS (MOUSE).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE.
RX   STRAIN=A/J;
RX   MEDLINE; 82150934.
RA   SIEGELMAN M., CAPRA J.D.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC   -!- ANTI-ARSONATE HYBRIDOMA PROTEIN.
CC   PIR; A01927; KVMSAR.
DR   HSSP; P01607; 1FAI.
KW   IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT   DOMAIN         1     23       FRAMEWORK 1.
FT   DOMAIN        24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN        35     49       FRAMEWORK 2.
FT   DOMAIN        50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN        57     88       FRAMEWORK 3.
FT   DOMAIN        89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN        98    108       FRAMEWORK 4.
FT   DISULFID      23     88       BY SIMILARITY.
FT   NON_TER      108    108
SQ   SEQUENCE    108 AA;   11965 MW;   84754175 CRC32;

Query Match              58.0%;  Score 76;   DB 1;  Length 108;
Best Local Similarity    69.2%;  Pred. No. 1.10e-02;
Matches    9;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   53 LHWLQQEPDGTIK 65
        |:| || |||||:|
Db   33 LNWYQQKPDGTVK 45


RESULT 9
ID   YCAJ_ECOLI   STANDARD;      PRT;   447 AA.
AC   P45526; P75833;
DT   01-NOV-1995 (REL. 32, CREATED)
DT   01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   HYPOTHETICAL 49.6 KD PROTEIN IN LOLA-SERS INTERGENIC REGION.

Query Match              53.4%;  Score 70;   DB 1;  Length 108;
Best Local Similarity    61.5%;  Pred. No. 1.38e-01;
Matches    8;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   53 LHWLQQEPDGTIK 65
        |:| ||  ||||:|
Db   45 LNWYQRKPDGTVK 57
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GN YCAJ.
OS ESCHERICHIA COLI.
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
OC ENTEROBACTERIACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RA BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN [2]
RP SEQUENCE OF 1-61 FROM N.A.
RC STRAIN=K12 / MC4100;
RX MEDLINE; 95554654.
RA MATSUYAMA S.-I., TAJIMA T., TOKUDA H.;
RL EMBO J. 14:3365-3372(1995).
RN [3]
RP SEQUENCE OF 367-447 FROM N.A.
RC STRAIN=K12;
RX MEDLINE; 87146412.
RA HAERTLEIN M., MADERN D., LEBERMAN R.;
RL NUCLEIC ACIDS RES. 15:1005-1017(1987).
RN [4]
RP IDENTIFICATION.
RX MEDLINE; 96032851.
RA BORODOVSKY M., MCININCH J., KOONIN E.V., RUDD K.E., MEDIGUE C.,
RA DANCHIN A.;
RL NUCLEIC ACIDS RES. 23:3554-3562(1995).
CC -!- SIMILARITY: STRONG, TO H.INFLUENZAE HI1590 AND C.BURNETII HOMOLOG.
CC -!- SIMILARITY: TO YEAST YNL218W.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC   FRAMESHIFT IN POSITION 370.
DR EMBL; AE000191; G1787119; -.
DR EMBL; D49398; -; NOT_ANNOTATED_CDS.
DR EMBL; X05017; -; NOT_ANNOTATED_CDS.
DR ECOGENE; EG12690; YCAJ.
KW HYPOTHETICAL PROTEIN; ATP-BINDING.
FT NP_BIND   57   64   ATP (POTENTIAL).
SQ SEQUENCE   447 AA; 49626 MW; 0E657B5D CRC32;

Query Match   51.1%; Score 67; DB 1; Length 447;
Best Local Similarity   44.4%; Pred. No. 4.70e-01;
Matches   8; Conservative   5; Mismatches   4; Indels   1; Gaps   1;

Db   428 GEKLAWLAEQDQNSPIKR 445
             |::||| :|: :||||
Qy   50 GINLHWL-QOEPDGTIKR 66

RESULT 11
ID HEMA_IAHPR   STANDARD;   PRT;   570 AA.
AC P26101;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE HEMAGGLUTININ PRECURSOR.
GN HA.
OS INFLUENZA A VIRUS (STRAIN A/EQUINE/PRAGUE/1/56).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92230399.
RA GIBSON C.A., DANIELS R.S., OXFORD J.S., MCCAULEY J.W.;
RL VIRUS RES. 22:93-106(1992).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC   CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO CHAINS
CC   (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
DR EMBL; X62552; G59204; -.
DR PIR; A45591; A45591.
HSSP; P03437; 1HGD.
KW ENVELOPE PROTEIN; HEMAGGLUTININ; GLYCOPROTEIN; SIGNAL.
FT SIGNAL   1   18
FT CHAIN   19   345   HA1 CHAIN.
FT CHAIN   346   570   HA2 CHAIN.
FT CARBOHYD   30   30   POTENTIAL.
FT CARBOHYD   46   46   POTENTIAL.
FT CARBOHYD   167   167   POTENTIAL.
FT CARBOHYD   249   249   POTENTIAL.
FT CARBOHYD   431   431   POTENTIAL.
FT CARBOHYD   503   503   POTENTIAL.
SQ SEQUENCE   570 AA; 64139 MW; 399E8F59 CRC32;

Query Match   51.1%; Score 67; DB 1; Length 570;
Best Local Similarity   42.9%; Pred. No. 4.70e-01;
Matches   6; Conservative   5; Mismatches   3; Indels   0; Gaps   0;

Db   239 IDFHWIMLDPNDTV 252
             |::||| :|: :|
Qy   51 INLHWLQOEPDGTI 64

RESULT 12
ID UFO2_MANES   STANDARD;   PRT;   346 AA.
AC Q40285;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE FLAVONOL 3-O-GLUCOSYLTRANSFERASE 2 (EC 2.4.1.91) (UDP-GLUCOSE
DE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 2) (FRAGMENT).
GN GT2 OR UGT73A2.
OS MANIHOT ESCULENTA (CASSAVA) (MANIOC).
OC EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
OC EUPHORBIALES; EUPHORBIACEAE;
RN [1]

RESULT 10
ID HEMA_IAHC6   STANDARD;   PRT;   570 AA.
AC P26094;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE HEMAGGLUTININ PRECURSOR.
HA.
OS INFLUENZA A VIRUS (STRAIN A/EQUINE/CAMBRIDGE/1/63).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92230399.
RA GIBSON C.A., DANIELS R.S., OXFORD J.S., MCCAULEY J.W.;
RL VIRUS RES. 22:93-106(1992).
CC -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC   CELL RECEPTORS AND FOR INITIATING INFECTION.
CC -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO CHAINS
CC   (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
EMBL; X62553; G59190; -.
PIR; S22013; S22013.
HSSP; P03437; 1HGD.
KW ENVELOPE PROTEIN; HEMAGGLUTININ; GLYCOPROTEIN; SIGNAL.
SIGNAL   1   18
CHAIN   19   345   HA1 CHAIN.
CHAIN   346   570   HA2 CHAIN.
CARBOHYD   30   30   POTENTIAL.
CARBOHYD   46   46   POTENTIAL.
CARBOHYD   249   249   POTENTIAL.
CARBOHYD   431   431   POTENTIAL.
CARBOHYD   503   503   POTENTIAL.
SEQUENCE   570 AA; 64151 MW; E4F3F882 CRC32;

Query Match   51.1%; Score 67; DB 1; Length 570;
Best Local Similarity   42.9%; Pred. No. 4.70e-01;
Matches   6; Conservative   5; Mismatches   3; Indels   0; Gaps   0;

Db   239 IDFHWIMLDPNDTV 252
             |::||| :|: :|
Qy   51 INLHWLQOEPDGTI 64

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RP   SEQUENCE FROM N.A.
RC   TISSUE-COTYLEDON;
RX   MEDLINE; 95201291.
RA   HUGHES J., HUGHES M.A.;
RL   DNA SEQ. 5:41-49(1994).
CC   -!- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, THIS
CC       GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYANIN
CC       PIGMENTS (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: UDP-GLUCOSE + A FLAVONOL = UDP + FLAVONOL
CC       3-O-D-GLUCOSIDE.
CC   -!- PATHWAY: ONE OF THE ESSENTIAL AND TERMINAL STEPS IN THE
CC       ANTHOCYANIN BIOSYNTHETIC PATHWAY.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN COTYLEDONS, ROOTS AND LEAVES.
CC   -!- DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION IN COTYLEDONS THAT JUST
CC       EMERGED FROM THE SEED COAT. LOW LEVELS IN HYPOCOTYLS AND
CC       INCREASING LEVELS IN ROOTS THROUGHOUT THIS PERIOD OF DEVELOPMENT.
CC   -!- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
DR   EMBL; X77461; G452255; -.
RP   PROSITE; PS00375; UDPGT; 1.
     TRANSFERASE; GLYCOSYLTRANSFERASE; MULTIGENE FAMILY.
NON_TER        1      1
SQ   SEQUENCE   346 AA;  38834 MW;  6E8242F0 CRC32;

Query Match             Best Local Similarity 33.3%;
     Score 66;  DB 1;  Length 346;
Matches    4;  Conservative    8;  Pred. No. 7.02e-01;  Indels   0;  Gaps   0;

Db  136 MQWLDDQPEGSSV 147
        ::||:||:|:|:|
Qy   53 LHWLQQEPDGTI 64


RESULT 13
ID   VSI3_REOVL     STANDARD;      PRT;   365 AA.
AC   P07939;
DT   01-AUG-1988 (REL. 08, CREATED)
DT   01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
DT   01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
DE   SIGMA 3 PROTEIN (MAJOR OUTER CAPSID PROTEIN).
GN   S4.
OS   REOVIRUS (TYPE 1 / STRAIN LANG).
OC   VIRIDAE; DS-RNA NONENVELOPED VIRUSES; REOVIRIDAE; REOVIRUSES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 86215171.
RA   ATWATER J.A., MANEMITSU S.M., SAMUEL C.E.;
RL   BIOCHEM. BIOPHYS. RES. COMMUN. 136:183-192(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92142506.
RA   SELIGER L.S., GIANTINI M., SHATKIN A.J.;
RL   VIROLOGY 187:202-210(1992).
CC   -!- FUNCTION: THE VIRAL OUTER SHELL POLYPEPTIDES, OF WHICH SIGMA 3 IS
CC       ONE, IMPOSE STRUCTURAL CONSTRAINTS THAT PREVENT ELONGATION OF
CC       NASCENT TRANSCRIPTS BY THE VIRION-ASSOCIATED RNA-POLYMERASE.
CC       SIGMA-3 ALSO INHIBITS HOST PROTEIN SYNTHESIS IN INFECTED MOUSE L
CC       CELLS AND MAY BE INVOLVED IN SWITCHING FROM CELLULAR TO VIRAL MRNA
CC       TRANSLATION AT LATE TIMES AFTER INFECTION.
DR   EMBL; M11139; G333720; -.
DR   EMBL; X61586; G61948; -.
DR   PIR; A24245; MNXRS4.
DR   PIR; A42192; A42192.
KW   COAT PROTEIN.
FT   CONFLICT    325    325       D -> N (IN REF. 2).
SQ   SEQUENCE   365 AA;  41156 MW;  B001989A CRC32;

Query Match             Best Local Similarity 33.3%;
     Score 66;  DB 1;  Length 365;
Matches    5;  Conservative    8;  Pred. No. 8;  Mismatches 2;  Indels   0;  Gaps   0;

Db  129 VELNWLQVDPNSMFR 143
        :|:||:|||.|:||:||
Qy   51 INLHWLQQEPDGIK 65
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RESULT 14
ID   HEMA_IATKR     STANDARD;      PRT;   560 AA.
AC   P03458;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   HEMAGGLUTININ PRECURSOR.
HA.
OS   INFLUENZA A VIRUS (STRAIN A/TURKEY/OREGON/71).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90266469.
RA   ORLICH M., KHATCHIKIAN D., TEIGLER A., ROTT R.;
RL   VIROLOGY 176:531-538(1990).
RN   [2]
RP   SEQUENCE OF 1-108 FROM N.A.
RX   MEDLINE; 82150925.
RA   AIR G.M.;
RL   PROC. NATL. ACAD. SCI. U.S.A. 78:7639-7643(1981).
CC   -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC       CELL RECEPTORS AND FOR INITIATING INFECTION.
CC   -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO CHAINS
CC       (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
DR   EMBL; M31689; G323975; -.
DR   EMBL; J02164; G324163; -.
DR   PIR; A34772; HMIVT7.
DR   PIR; A04069; A04069.
     HSSP; P03437; 1HGD.
KW   ENVELOPE PROTEIN; HEMAGGLUTININ; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     18
FT   CHAIN        19    338       HA1 CHAIN.
FT   CHAIN       340    560       HA2 CHAIN.
FT   CARBOHYD     30     30       POTENTIAL.
FT   CARBOHYD     46     46       POTENTIAL.
FT   CARBOHYD    249    249       POTENTIAL.
FT   CARBOHYD    421    421       POTENTIAL.
FT   CARBOHYD    493    493       POTENTIAL.
FT   CONFLICT     60     60       S -> C (IN REF. 2).
FT   CONFLICT     92     92       S -> L (IN REF. 2).
FT   CONFLICT    103    103       D -> N (IN REF. 2).
SQ   SEQUENCE   560 AA;  62013 MW;  74DE95A9 CRC32;

Query Match             Best Local Similarity 42.9%;
     Score 66;  DB 1;  Length 560;
Matches    6;  Conservative    5;  Pred. No. 7.02e-01;  Mismatches 3;  Indels   0;  Gaps   0;

Db  239 IDFHWLLLDPNDTV 252
        |::||:|:|:|
Qy   51 INLHWLQQEPDGTI 64


RESULT 15
ID   HEMA_IAFPR     STANDARD;      PRT;   563 AA.
AC   P03459;
DT   21-JUL-1986 (REL. 01, CREATED)
DT   21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT   01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE   HEMAGGLUTININ PRECURSOR.
HA.
OS   INFLUENZA A VIRUS (STRAIN A/FOWL PLAGUE VIRUS/ROSTOCK/34).
OC   VIRIDAE; SS-RNA ENVELOPED VIRUSES; NEGATIVE-STRAND; ORTHOMYXOVIRIDAE.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 80054765.
RA   PORTER A.G., BARBER C., CAREY N.H., HALLEWELL R.A., THRELFALL G.,
RA   EMTAGE J.S.;
RL   NATURE 282:471-477(1979).
RN   [2]
RP   MUTANTS TS1 AND TS227.
RX   MEDLINE; 87080266.
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RA   SCHUY W., WILL C., KURODA K., SCHOLTISSEK C., GARTEN W., KLENK H.-D.;
RL   EMBO J. 5:2831-2836(1986).
RN   [3]
RP   STRUCTURE OF CARBOHYDRATES ON ASN-424 AND ASN-496.
RA   GEYER R., DIABATE S., GEYER H., KLENK H.-D., NIEMANN H., STIRM S.;
RL   GLYCOCONJ. J. 4:17-32(1987).
CC   -!- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO
CC       CELL RECEPTORS AND FOR INITIATING INFECTION.
CC   -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMER IS FORMED BY TWO CHAINS
CC       (HA1 AND HA2) LINKED BY A DISULFIDE BOND.
CC   -!- PTM: CLEAVAGE OF HEMAGGLUTININ INTO TWO SUBUNITS, HA1 AND HA2,
CC       USUALLY TAKES PLACE EITHER ON SMOOTH INTERNAL MEMBRANES OR AT
CC       THE PLASMA MEMBRANE; THIS STEP IS ESSENTIAL FOR INFECTIVITY AND
CC       PROBABLY ALSO FOR PATHOGENICITY.
CC   -!- MUTANTS TS1 AND TS227 HAVE A TEMPERATURE SENSITIVE DEFECT IN
CC       THE TRANSPORT OF THE HEMAGGLUTININ FROM THE ROUGH ENDOPLASMIC
CC       RETICULUM TO THE GOLGI APPARATUS.
DR   EMBL; V01105; G60807; -.
     PIR; A04070; HMIVF.
     HSSP; P03437; 1HGD.
     ENVELOPE PROTEIN; HEMAGGLUTININ; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     18
FT   CHAIN        19    336       HA1 CHAIN.
FT   PROPEP      337    342       CONNECTING PEPTIDE.
FT   CHAIN       343    563       HA2 CHAIN.
FT   CARBOHYD     30     30
FT   CARBOHYD     46     46
FT   CARBOHYD    141    141
FT   CARBOHYD    167    167
FT   CARBOHYD    249    249
FT   CARBOHYD    424    424       OLIGOMANNOSIDIC.
FT   CARBOHYD    475    475       IN MUTANT_TS227.
FT   CARBOHYD    496    496       OLIGOMANNOSIDIC.
FT   VARIANT     113    113       E -> G (IN MUTANT TS227).
FT   VARIANT     293    293       S -> G (IN MUTANT TS1).
FT   VARIANT     416    416       E -> G (IN MUTANT TS1).
FT   VARIANT     475    475       D -> N (IN MUTANT TS227).
SQ   SEQUENCE    563 AA;   62702 MW;  E543081E CRC32.

Db  239 IDFHWLILDPNDTV 252
            |:|||  :|: |:
Qy   51 INLHWLQQEPDGTI 64

Query Match    49.6%;   Score 65;  DB 1;  Length 563;
Best Local Similarity   42.9%;   Pred. No. 1.04e+00;
Matches    6;  Conservative    5;  Mismatches   3;  Indels   0;  Gaps   0;

Match completed: Tue Apr 20 13:57:38 1999
Job time : 7 secs.
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